

Sir:

12/01/97

[illegible]

For: NOVEL EXPRESSION VECTORS CONTAINING ACCESSORY MOLECULE
LIGAND GENES AND THEIR USE FOR IMMUNOMODULATION AND
TREATMENT OF MALIGNANCIES AND AUTOIMMUNE DISEASE

X 110 page(s) specification; 8 page(s) claims;
 1 page(s) abstract.

X 30 sheets of drawings (X informal formal)

X Declaration and Power of Attorney (_ signed X unsigned)

_____ Assignment of the invention to: _____

_____ Certified copy(s) of priority documents ()

X A Verified Statement Claiming Small Entity Status under
 37 CFR §1.9 and §1.27.

X Sequence Listing and Statement and Sequence Listing.

_____ Preliminary Amendment

I hereby certify that this paper (along with any referred to as being attached or enclosed) is being deposited with the United States Postal Service on the date shown below with sufficient postage as Express Mail in an envelope addressed to the Assistant Commissioner for Patents, Washington, D.C. 20231.

name of person mailing paper
Joseph M. Olivera
signature of person mailing paper

The filing fee has been calculated as shown below:

-Statutory Basic Filing Fee		(\$790)	\$ 790.00
-Total Claims	<u>83</u>	(-20 <u>63</u> x \$22)	\$1,386.00
-Independent Claims	<u>17</u>	(-3 <u>14</u> x \$82)	\$1,148.00
-Multiple Dependent Claim(s)		(\$270)	\$ 270.00
-Surcharge 37 CFR 1.16(e)		(\$130)	\$ 0.00
TOTAL OF ABOVE CALCULATIONS			\$3,594.00
-Reduction for Small Entity (1/2)			\$1,797.00
-Assignment		(\$40)	\$ 0.00
TOTAL FEES SUBMITTED HEREWITH			\$1,797.00

_____ This application is filed without fee or signed declaration pursuant to 37 CFR \$1.53.

X A check in the amount of \$1,797.00 to cover the above fees is enclosed.

X The Commissioner is hereby authorized to charge payment of the fees associated with this communication, or credit any overpayment, to Deposit Account 12-2475. A duplicate copy of this sheet is enclosed.

Respectfully Submitted

LYON & LYON

Dated: 12/1/97

Jeff W. Guise
Jeffrey W. Guise
Reg. No. 34,613

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Address all correspondence to Jeffrey W. Guise, Esq., LYON & LYON, 633 West Fifth Street, Suite 4700, Los Angeles, CA 90071-2066.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patents issuing thereon.

Full name of sole or first inventor Thomas J. Kipps

Inventor's signature _____ Date: _____

Residence 731 Fresca Court, Solana Beach, CA 92075 Citizenship United States

Post Office Address Same as above

Full name of second inventor Sanjai Sharma

Inventor's signature _____ Date: _____

Residence 11478 Duenda Road, San Diego, CA 92127 Citizenship India

Post Office Address Same as above

Full name of third inventor Mark Cantwell

Inventor's signature _____ Date: _____

Residence 7015 Charmant Drive, #243, San Diego, CA 92122 Citizenship United States

Post Office Address Same as above

Applicant or Patentee: Kipps et al.
Serial or Patent No.: Unassigned
Filed or Issued: Filed Herewith
For: NOVEL EXPRESSION VECTORS CONTAINING ACCESSORY MOLECULE LIGAND
GENES AND THEIR USE FOR IMMUNOMODULATION AND TREATMENT OF
MALIGNANCIES AND AUTOIMMUNE DISEASE

**VERIFIED STATEMENT (DECLARATION) CLAIMING SMALL ENTITY STATUS
(37 CFR 1.9(e) and 1.27(d)) - NONPROFIT ORGANIZATION**

I hereby declare that I am an official empowered to act on behalf of the nonprofit organization identified below:

NAME OF ORGANIZATION: UNIVERSITY OF CALIFORNIA
ADDRESS OF ORGANIZATION: Technology Transfer Office
9500 Gilman Drive
La Jolla, CA 92093

TYPE OF ORGANIZATION:

- ☒ UNIVERSITY OR OTHER INSTITUTION OF HIGHER EDUCATION
☐ TAX EXEMPT UNDER INTERNAL REVENUE SERVICE CODE (26 USC 501(a) and 501(c)(3))
☐ NONPROFIT SCIENTIFIC OR EDUCATIONAL UNDER STATUTE OF STATE OF THE UNITED STATES
OF AMERICA
(NAME OF STATE:)
(CITATION OF STATUTE:)
☐ WOULD QUALIFY AS TAX EXEMPT UNDER INTERNAL REVENUE SERVICE CODE (26 USC 501(a) and
501(c)(3)) IF LOCATED IN THE UNITED STATES OF AMERICA
☐ WOULD QUALIFY AS NONPROFIT SCIENTIFIC OR EDUCATIONAL UNDER STATUTE OF STATE OF
THE UNITED STATES OF AMERICA IF LOCATED IN THE UNITED STATES OF AMERICA
(NAME OF STATE:)
(CITATION OF STATUTE:)

I hereby declare that the nonprofit organization identified above qualifies as a nonprofit organization as defined
in 37 CFR 1.9(e) for purposes of paying reduced fees under section 41(a) and (b) of Title 35, United States Code,
with regard to the invention entitled NOVEL EXPRESSION VECTORS CONTAINING ACCESSORY MOLECULE
LIGAND GENES AND THEIR USE FOR IMMUNOMODULATION AND TREATMENT OF MALIGNANCIES
AND AUTOIMMUNE DISEASE by inventor(s) Kipps et al. described in

- ☒ the specification filed herewith.
☐ application serial no. _____, filed _____.
☐ patent no. _____, issued _____.

I hereby declare that rights under contract or law have been conveyed to and remain with the nonprofit
organization with regard to the above identified invention.

If the rights held by the nonprofit organization are not exclusive, each individual, concern or organization having
rights to the invention is listed below* and no rights to the invention are held by any person, other than the
inventor, who could not qualify as a small business concern under 37 CFR 1.9(d) or by any concern which
would not qualify as a small business concern under 37 CFR 1.9(d) or a nonprofit organization under 37 CFR
1.9(e).

**NOTE: Separate verified statements are required from each named person, concern or organization having
rights to the invention averring to their status as small entities. (37 CFR 1.27)*

NAME _____
ADDRESS _____
☐ INDIVIDUAL ☐ SMALL BUSINESS CONCERN ☐ NONPROFIT ORGANIZATION

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants:)	Group Art Unit:
Thomas J. Kipps et al.)	Examiner:
Serial No. To Be Assigned)	
Filed: Herewith)	
For: NOVEL EXPRESSION VECTORS)	
CONTAINING ACCESSORY)	
MOLECULE LIGAND GENES AND)	
THEIR USE FOR IMMUNO-)	
MODULATION AND TREATMENT OF)	
MALIGNANCIES)	

STATEMENT UNDER 37 C.F.R. § 1.821 (F)

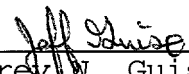
Assistant Commissioner of Patents
Washington, D.C. 20231

Sir:

I hereby state that the content of the paper and computer readable copies of the Sequence Listing, submitted in accordance with 37 C.F.R. § 1.821 (e), (f) and (g), or § 1.825 (d) and (b) respectively, are the same.

Respectfully submitted,

LYON & LYON LLP



Jeffrey W. Guise
Registration No. 34,613

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CERTIFICATE OF MAILING

I hereby certify that this paper (along with any referred to as being attached or enclosed) is being deposited with the United States Postal Service on the date shown below with sufficient postage as Express Mail in an envelope addressed to the Assistant Commissioner for Patents, Washington, D.C. 20231.

TB608349181US
Express Mail mailing no.
December 1, 1997
date of deposit

Jeanette M. Olivera
name of person mailing paper
Jeanette M. Olivera
signature of person mailing paper

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/132145
(B) FILING DATE: 12/9/96

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Guise, Jeffrey W.
(B) REGISTRATION NUMBER: 34,613
(C) REFERENCE/DOCKET NUMBER: 231/003

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (213) 489-1600
(B) TELEFAX: (213) 955-0440
(C) TELEX: 67-3510

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 786 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATGATCGAAA	CATACAACCA	AACTTCTCCC	CGATCTGCGG	CCACTGGACT	GCCCATCAGC	60
ATGAAAAATTT	TTATGTATTT	ACTTACTGTT	TTTCTTATCA	CCCAGATGAT	TGGGTCAGCA	120
CTTTTTGCTG	TGTATCTTCA	TAGAAGGTTG	GACAAGATAG	AAGATGAAAG	GAATCTTCAT	180
GAAGATTTTG	TATTCATGAA	AACGATACAG	AGATGCAACA	CAGGAGAAAG	ATCCTTATCC	240
TTACTGAACT	GTGAGGAGAT	TAAAAGCCAG	TTTGAAGGCT	TTGTGAAGGA	TATAATGTTA	300
AACAAAGAGG	AGACGAAGAA	AGAAAACAGC	TTTGAAATGC	AAAAAGGTGA	TCAGAATCCT	360
CAAATTGCGG	CACATGTCAT	AAGTGAGGCC	AGCAGTAAAA	CAACATCTGT	GTTACAGTGG	420
GCTGAAAAAG	GATACTACAC	CATGAGCAAC	AACTTGGTAA	CCCTGGAAAA	TGGGAAACAG	480
CTGACCGTTA	AAAGACAAGG	ACTCTATTAT	ATCTATGCCC	AAGTCACCTT	CTGTTCCAAT	540
CGGGAAGCTT	CGAGTCAAGC	TCCATTTATA	GCCAGCCTCT	GCCTAAAGTC	CCCCGGTAGA	600
TTCGAGAGAA	TCTTACTCAG	AGCTGCAAAT	ACCCACAGTT	CCGCCAAACC	TTGCGGGCAA	660
CAATCCATTC	ACTTGGGAGG	AGTATTTGAA	TTGCAACCAG	GTGCTTCGGT	GTTTGTCAAT	720
GTGACTGATC	CAAGCCAAGT	GAGCCATGGC	ACTGGCTTCA	CGTCCTTTGG	CTTACTCAA	780
CTCTGA						786

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 783 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATGATAGAAA	CATACAGCCA	ACCTTCCCCC	AGATCCGTGG	CAACTGGACT	TCCAGCGAGC	60
ATGAAGATTT	TTATGTATTT	ACTTACTGTT	TTCTTATCA	CCCAAATGAT	TGGATCTGTG	120
CTTTTGTCTG	TGTATCTTCA	TAGAAGATTG	GATAAGGTCG	AAGAGGAAGT	AAACCTTCAT	180
GAAGATTTTG	TATTCATAAA	AAAGCTAAAG	AGATGCAACA	AAGGAGAAGG	ATCTTTATCC	240
TTGCTGAACT	GTGAGGAGAT	GAGAAGGCAA	TTTGAAGACC	TTGTCAAGGA	TATAACGTTA	300
AACAAAGAAG	AGAAAAAAGA	AAACAGCTTT	GAAATGCAAA	GAGGTGATGA	GGATCCTCAA	360
ATTGCAGCAC	ACGTTGTAAG	CGAAGCCAAC	AGTAATGCAG	CATCCGTTCT	ACAGTGGGCC	420
AAGAAAGGAT	ATTATACCAT	GAAAAGCAAC	TTGGTAATGC	TTGAAAATGG	GAAACAGCTG	480
ACGGTTAAAA	GAGAAGGACT	CTATTATGTC	TACACTCAAG	TCACCTTCTG	CTCTAATCGG	540
GAGCCTTCGA	GTCAACGCCC	ATTTCATCGTC	GGCCTCTGGC	TGAAGCCCAG	CATTGGATCT	600
GAGAGAATCT	TACTCAAGGC	GGCAAATACC	CACAGTTCCT	CCCAGCTTTG	CGAGCAGCAG	660
TCTGTTCACT	TGGGCGGAGT	GTTTGAATTA	CAAGCTGGTG	CTTCTGTGTT	TGTCAACGTG	720
ACTGAAGCAA	GCCAAGTGAT	CCACAGAGTT	GGCTTCTCAT	CTTTTGGCTT	ACTCAAATC	780
TGA						783

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 783 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATGATCGAAA	CATACAACCA	AACTTCTCCC	CGATCTGCGG	CCACTGGACT	GCCCATCAGC	60
ATGAAAATTT	TTATGTATTT	ACTTACTGTT	TTTCTTATCA	CCCAGATGAT	TGGGTCAGCA	120
CTTTTGTCTG	TGTATCTTCA	TAGAAGATTG	GATAAGGTCG	AAGAGGAAGT	AAACCTTCAT	180
GAAGATTTTG	TATTCATAAA	AAAGCTAAAG	AGATGCAACA	AAGGAGAAGG	ATCTTTATCC	240
TTGCTGAACT	GTGAGGAGAT	GAGAAGGCAA	TTTGAAGACC	TTGTCAAGGA	TATAACGTTA	300
AACAAAGAAG	AGAAAAAAGA	AAACAGCTTT	GAAATGCAAA	GAGGTGATGA	GGATCCTCAA	360
ATTGCAGCAC	ACGTTGTAAG	CGAAGCCAAC	AGTAATGCAG	CATCCGTTCT	ACAGTGGGCC	420
AAGAAAGGAT	ATTATACCAT	GAAAAGCAAC	TTGGTAATGC	TTGAAAATGG	GAAACAGCTG	480
ACGGTTAAAA	GAGAAGGACT	CTATTATGTC	TACACTCAAG	TCACCTTCTG	CTCTAATCGG	540
GAGCCTTCGA	GTCAACGCCC	ATTTCATCGTC	GGCCTCTGGC	TGAAGCCCAG	CATTGGATCT	600
GAGAGAATCT	TACTCAAGGC	GGCAAATACC	CACAGTTCCT	CCCAGCTTTG	CGAGCAGCAG	660
TCTGTTCACT	TGGGCGGAGT	GTTTGAATTA	CAAGCTGGTG	CTTCTGTGTT	TGTCAACGTG	720
ACTGAAGCAA	GCCAAGTGAT	CCACAGAGTT	GGCTTCTCAT	CTTTTGGCTT	ACTCAAATC	780
TGA						783

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 786 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ATGATCGAAA	CATACAACCA	AACTTCTCCC	CGATCTGCGG	CCACTGGACT	GCCCATCAGC	60
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ATGAAAATTT	TTATGTATTT	ACTTACTGTT	TTCCTTATCA	CCCAAATGAT	TGGATCTGTG	120
CTTTTTGCTG	TGTATCTTCA	TAGAAGGTTG	GACAAGATAG	AAGATGAAAG	GAATCTTCAT	180
GAAGATTTTG	TATTCATGAA	AACGATACAG	AGATGCAACA	CAGGAGAAAG	ATCCTTATCC	240
TTACTGAACT	GTGAGGAGAT	TAAAAGCCAG	TTTGAAGGCT	TTGTGAAGGA	TATAATGTTA	300
AACAAAGAGG	AGACGAAGAA	AGAAAACAGC	TTTGAAATGC	AAAAAGGTGA	TCAGAATCCT	360
CAAATTGCGG	CACATGTCAT	AAGTGAGGCC	AGCAGTAAAA	CAACATCTGT	GTTACAGTGG	420
GCTGAAAAAG	GATACTACAC	CATGAGCAAC	AACTTGGTAA	CCCTGGAAAA	TGGGAAACAG	480
CTGACCGTTA	AAAGACAAGG	ACTCTATTAT	ATCTATGCCC	AAGTCACCTT	CTGTTCCAAT	540
CGGGAAGCTT	CGAGTCAAGC	TCCATTTATA	GCCAGCCTCT	GCCTAAAGTC	CCCCGGTAGA	600
TTCGAGAGAA	TCTTACTCAG	AGCTGCAAAT	ACCCACAGTT	CCGCCAAACC	TTGCGGGCAA	660
CAATCCATTC	ACTTGGGAGG	AGTATTTGAA	TTGCAACCAG	GTGCTTCGGT	GTTTGTCAAT	720
GTGACTGATC	CAAGCCAAGT	GAGCCATGGC	ACTGGCTTCA	CGTCCTTTGG	CTTACTCAAA	780
CTCTGA						786

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 783 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATGATCGAAA	CATACAACCA	AACTTCTCCC	CGATCTGCGG	CCACTGGACT	GCCCATCAGC	60
ATGAAAATTT	TTATGTATTT	ACTTACTGTT	TTCCTTATCA	CCCAAATGAT	TGGATCTGTG	120
CTTTTTGCTG	TGTATCTTCA	TAGAAGATTG	GATAAGGTCG	AAGAGGAAGT	AAACCTTCAT	180
GAAGATTTTG	TATTCATAAA	AAAGCTAAAG	AGATGCAACA	AAGGAGAAGG	ATCTTTATCC	240
TTGCTGAACT	GTGAGGAGAT	GAGAAGGCAA	TTTGAAGACC	TTGTCAAGGA	TATAACGTTA	300
AACAAAGAAG	AGAAAAAAGA	AAACAGCTTT	GAAATGCAAA	GAGGTGATGA	GGATCCTCAA	360
ATTGCAGCAC	ACGTTGTAAG	CGAAGCCAAC	AGTAATGCAG	CATCCGTTCT	ACAGTGGGCC	420
AAGAAAGGAT	ATTATACCAT	GAAAAGCAAAC	TTGGTAATGC	TTGAAAATGG	GAAACAGCTG	480
ACGGTTAAAA	GAGAAGGACT	CTATTATGTC	TACACTCAAG	TCACCTTCTG	CTCTAATCGG	540
GAGCCTTCGA	GTCAACGCCC	ATTTCATCGTC	GGCCTCTGGC	TGAAGCCCAG	CATTGGATCT	600
GAGAGAATCT	TACTCAAGGC	GGCAAATACC	CACAGTTCCT	CCCAGCTTTG	CGAGCAGCAG	660
TCTGTTCACT	TGGGCGGAGT	GTTTGAATTA	CAAGCTGGTG	CTTCTGTGTT	TGTCAACGTG	720
ACTGAAGCAA	GCCAAGTGAT	CCACAGAGTT	GGCTTCTCAT	CTTTTGGCTT	ACTCAAACCT	780
TGA						783

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 786 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

ATGATAGAAA	CATACAGCCA	ACCTTCCCCC	AGATCCCGTGG	CAACTGGACT	TCCAGCGAGC	60
ATGAAGATTT	TTATGTATTT	ACTTACTGTT	TTTCTTATCA	CCCAGATGAT	TGGGTCAGCA	120
CTTTTTGCTG	TGTATCTTCA	TAGAAGGTTG	GACAAGATAG	AAGATGAAAG	GAATCTTCAT	180
GAAGATTTTG	TATTCATGAA	AACGATACAG	AGATGCAACA	CAGGAGAAAG	ATCCTTATCC	240
TTACTGAACT	GTGAGGAGAT	TAAAAGCCAG	TTTGAAGGCT	TTGTGAAGGA	TATAATGTTA	300

AACAAAGAGG	AGACGAAGAA	AGAAAACAGC	TTTGAAATGC	AAAAAGGTGA	TCAGAATCCT	360
CAAATTGCGG	CACATGTCAT	AAGTGAGGCC	AGCAGTAAAA	CAACATCTGT	GTTACAGTGG	420
GCTGAAAAAG	GATACTACAC	CATGAGCAAC	AACTTGGTAA	CCCTGGAAAA	TGGGAAACAG	480
CTGACCGTTA	AAAGACAAGG	ACTCTATTAT	ATCTATGCCC	AAGTCACCTT	CTGTTCCAAT	540
CGGGAAGCTT	CGAGTCAAGC	TCCATTTATA	GCCAGCCTCT	GCCTAAAGTC	CCCCGGTAGA	600
TTCGAGAGAA	TCTTACTCAG	AGCTGCAAAAT	ACCCACAGTT	CCGCCAAACC	TTGCGGGCAA	660
CAATCCATTC	ACTTGGGAGG	AGTATTTGAA	TTGCAACCAG	GTGCTTCGGT	GTTTGTCAAT	720
GTGACTGATC	CAAGCCAAGT	GAGCCATGGC	ACTGGCTTCA	CGTCCTTTGG	CTTACTCAAA	780
CTCTGA						786

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 786 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ATGATAGAAA	CATACAGCCA	ACCTTCCCCC	AGATCCGTGG	CAACTGGACT	TCCAGCGAGC	60
ATGAAGATTT	TTATGTATTT	ACTTACTGTT	TTCCTTATCA	CCCAAATGAT	TGGATCTGTG	120
CTTTTTCGCTG	TGTATCTTCA	TAGAAGGTTG	GACAAAGATAG	AAGATGAAAG	GAATCTTCAT	180
GAAGATTTTG	TATTCATGAA	AACGATACAG	AGATGCAACA	CAGGAGAAAG	ATCCTTATCC	240
TTACTGAACT	GTGAGGAGAT	TAAAAGCCAG	TTTGAAGGCT	TTGTGAAGGA	TATAATGTTA	300
AACAAAGAGG	AGACGAAGAA	AGAAAACAGC	TTTGAAATGC	AAAAAGGTGA	TCAGAATCCT	360
CAAATTGCGG	CACATGTCAT	AAGTGAGGCC	AGCAGTAAAA	CAACATCTGT	GTTACAGTGG	420
GCTGAAAAAG	GATACTACAC	CATGAGCAAC	AACTTGGTAA	CCCTGGAAAA	TGGGAAACAG	480
CTGACCGTTA	AAAGACAAGG	ACTCTATTAT	ATCTATGCCC	AAGTCACCTT	CTGTTCCAAT	540
CGGGAAGCTT	CGAGTCAAGC	TCCATTTTATA	GCCAGCCTCT	GCCTAAAGTC	CCCCGGTAGA	600
TTCGAGAGAA	TCTTACTCAG	AGCTGCAAAAT	ACCCACAGTT	CCGCCAAACC	TTGCGGGCAA	660
CAATCCATTC	ACTTGGGAGG	AGTATTTGAA	TTGCAACCAG	GTGCTTCGGT	GTTTGTCAAT	720
GTGACTGATC	CAAGCCAAGT	GAGCCATGGC	ACTGGCTTCA	CGTCCTTTGG	CTTACTCAAA	780
CTCTGA						786

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 864 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

AACTCTAACG	CAGCATGATC	GAAACATACA	GTCAACCTTC	TCCCCGCTCC	GTGGCCACTG	60
GACCACCTGT	CAGTATGAAA	ATTTTTATGT	ATTTACTTAC	AGTTTTTCTT	ATCACCAGAA	120
TGATTGGGTC	AGCGCTTTTT	GCTGTGTATC	TTCACAGACG	ATTGGACAAG	ATAGAAGACG	180

AAAGGAATCT	TCATGAAGAT	TTTGTGTTCA	TGAAAACGAT	ACAGAGATGC	AATAAAGGAG	240
AGGGGTCTTT	ATCCTTACTG	AACTGTGAGG	AAATTAGAAG	CCGGTTTGAA	GACTTGGTCA	300
AGGATATAAT	GCAAAACAAA	GAAGTAAAGA	AGAAAGAAAA	AAACTTTGAA	ATGCACAAGG	360
GTGATCAGGA	GCCTCAGATA	GCGGCACATG	TCATCAGTGA	GGCCAGTAGT	AAAACAACCT	420
CTGTTCTCCA	GTGGGCCCCC	AAAGGATACT	ACACCTTAAG	CAACAACCTG	GTAACCCTCG	480
AAAACGGGAA	ACAGCTGGCC	GTGAAAAGAC	AAGGATTCTA	TTACATCTAC	ACCCAAGTCA	540
CCTTCTGTTC	CAATCGGGAA	ACTTTGAGTC	AAGCTCCATT	TATAGCCAGC	CTCTGCCTGA	600
AGTCCCCAAG	TGGATCAGAG	AGAATCTTAC	TGAGAGCTGC	AAACACCCAC	AGTTCTTCCA	660
AACCATGCGG	GCAGCAATCC	ATTCACCTAG	GAGGAGTCTT	TGAATTGCAA	TCGGGTGCTT	720
CGGTGTTTGT	CAATGTGACT	GATCCAAGTC	AAGTGAGCCA	CGGGACGGGC	TTCACATCAT	780
TTGGCTTACT	CAAACTCTGA	ACGGTGTAAG	CCAGCAGGCT	GCGGCTGGGC	TGATGCTGGT	840
GGTCTTCACA	ATCCAGGAAA	GCAG				864

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3634 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GAATTCCGGG	TGATTTCACT	CCCGGCTGTC	CAGGCTTGTC	CTGCTACCCC	ACCCAGCCTT	60
TCCTGAGGCC	TCAAGCCTGC	CACCAAGCCC	CCAGCTCCTT	CTCCCCGCAG	GACCCAAACA	120
CAGGCCTCAG	GACTCAACAC	AGCTTTTCCC	TCCAACCCGT	TTTCTCTCCC	TCAACGGACT	180
CAGCTTCTG	AAGCCCCCTC	CAGTTCTAGT	TCTATCTTTT	TCCTGCATCC	TGTCTGGAAG	240
TTAGAAGGAA	ACAGACCACA	GACCTGGTCC	CCAAAAGAAA	TGGAGGCAAT	AGGTTTTGAG	300
GGGCATGGGG	ACGGGGTTCA	GCCTCCAGGG	TCCTACACAC	AAATCAGTCA	GTGGCCCAGA	360
AGACCCCCCT	CGGAATCGGA	GCAGGGAGGA	TGGGGAGTGT	GAGGGGTATC	CTTGATGCTT	420
GTGTGTCCCC	AACTTTCCAA	ATCCCCGCCC	CCGCGATGGA	GAAGAAACCG	AGACAGAAGG	480
TGCAGGGCCC	ACTACCGCTT	CCTCCAGATG	AGCTCATGGG	TTTCTCCACC	AAGGAAGTTT	540
TCCGCTGGTT	GAATGATTCT	TTCCCCGCCC	TCCTCTCGCC	CCAGGGACAT	ATAAAGGCAG	600
TTGTTGGCAC	ACCCAGCCAG	CAGACGCTCC	CTCAGCAAGG	ACAGCAGAGG	ACCAGCTAAG	660
AGGGAGAGAA	GCAACTACAG	ACCCCCCTG	AAAACAACCC	TCAGACGCCA	CATCCCCCTGA	720
CAAGCTGCCA	GGCAGGTTCT	CTTCCTCTCA	CATACTGACC	CACGGCTTCA	CCCTCTCTCC	780
CCTGGAAGG	ACACCATGAG	CACTGAAAGC	ATGATCCGGG	ACGTGGAGCT	GGCCGAGGAG	840
GCGCTCCCCA	AGAAGACAGG	GGGGCCCCAG	GGCTCCAGGC	GGTGCTTGTT	CCTCAGCCTC	900
TTCTCCTTCC	TGATCGTGGC	AGGCGCCACC	ACGCTCTTCT	GCCTGCTGCA	CTTTGGAGTG	960
ATCGGCCCCC	AGAGGGAAGA	GGTGAGTGCC	TGGCCAGCCT	TCATCCACTC	TCCCACCCAA	1020
GGGGAATGA	GAGACGCAAG	AGAGGGAGAG	AGATGGGATG	GGTGAAAGAT	GTGCGCTGAT	1080
AGGGAGGGAT	GAGAGAGAAA	AAAACATGGA	GAAAGACGGG	GATGCAGAAA	GAGATGTGGC	1140
AAGAGATGGG	GAAGAGAGAG	AGAGAAAGAT	GGAGAGACAG	GATGTCTGGC	ACATGGAAGG	1200
TGCTCACTAA	GTGTGTATGG	AGTGAATGAA	TGAATGAATG	AATGAACAAG	CAGATATATA	1260
AATAAGATAT	GGAGACAGAT	GTGGGGTGTG	AGAAGAGAGA	TGGGGGAAGA	AACAAGTGAT	1320
ATGAATAAAG	ATGGTGAGAC	AGAAAGAGCG	GGAAATATGA	CAGCTAAGGA	GAGAGATGGG	1380
GGAGATAAGG	AGAGAAGAAG	ATAGGGTGTC	TGGCACACAG	AAGACACTCA	GGGAAAGAGC	1440
TGTTGAATGC	TGGAAGGTGA	ATACACAGAT	GAATGGAGAG	AGAAAACCAG	ACACCTCAGG	1500
GCTAAGAGCG	CAGGCAGAC	AGGCAGCCAG	CTGTTCCTCC	TTTAAGGGTG	ACTCCCTCGA	1560
TGTTAACCAT	TCTCCTTCTC	CCCAACAGTT	CCCAAGGGAC	CTCTCTCTAA	TCAGCCCTCT	1620
GGCCCAGGCA	GTCAGTAAGT	GTCTCCAAAC	CTCTTTCTTA	ATTCTGGGTT	TGGGTTTGGG	1680
GGTAGGGTTA	GTACCGGTAT	GGAAGCAGTG	GGGGAATTTT	AAAGTTTTTG	TCTTGGGGGA	1740
GGATGGATGG	AGGTGAAAGT	AGGGGGGTAT	TTTCTAGGAA	GTTTAAGGGT	CTCAGCTTTT	1800
TCTTTTCTCT	CTCCTCTTCA	GGATCATCTT	CTCGAACCCC	GAGTGACAAG	CCTGTAGCCC	1860
ATGTTGTAGG	TAAGAGCTCT	GAGGATGTGT	CTTGGAACCT	GGAGGGCTAG	GATTTGGGGA	1920
TTGAAGCCCG	GCTGATGGTA	GGCAGAACTT	GGAGACAATG	TGAGAAGGAC	TCGCTGAGCT	1980
CAAGGGAAGG	GTGGAGGAAC	AGCACAGGCC	TTAGTGGGAT	ACTCAGAACG	TCATGGCCAG	2040

TGAAACAGCA	GTATCTTCTA	AGCCCTGGGG	GCTTCCCCGG	GCCCCAGCCC	CGACCTAGAA	1140
CCCGCCCGCT	GCCTGCCACG	CTGCCACTGC	CGCTTCTCT	ATAAAGGGAC	CTGAGCGTCC	1200
GGGCCCAGGG	GCTCCGCACA	GCAGGTGAGG	CTCTCCTGCC	CCATCTCCTT	GGGCTGCCCC	1260
TGCTTCGTGC	TTTGGACTAC	CGCCCAGCAG	TGTCCTGCCC	TCTGCCTGGG	CCTCGGTCCC	1320
TCCTGCACCT	GCTGCCTGGA	TCCCCGGCCT	GCCTGGGCCT	GGGCTTGGTG	GGTTTGGTTT	1380
TGGTTTCCTT	CTCTGTCTCT	GACTCTCCAT	CTGTCACTCT	CATTGTCTCT	GTCACACATT	1440
CTCTGTTTCT	GCCATGATTC	CTCTCTGTTC	CCTTCCTGTC	TCTCTCTGTC	TCCCTCTGCT	1500
CACCTTGGGG	TTTCTCTGAC	TGCATCTTGT	CCCCTTCTCT	GTCGATCTCT	CTCTCGGGGG	1560
TCGGGGGGTG	CTCTCTCCCA	GGGCGGGAGG	TCTGTCTTCC	GCCGCGTGCC	CCGCCCCGCT	1620
CACTGTCTCT	CTCTCTCTCT	CTCTTTCTCT	GCAGGTCTCT	CCCATGACAC	CACCTGAACG	1680
TCTCTTCTCT	CCAAGGGTGT	GTGGCACCAC	CCTACACCTC	CTCCTTCTGG	GGCTGCTGCT	1740
GGTCTGCTG	CCTGGGGCCC	AGGTGAGGCA	GCAGGAGAA	GGGGGCTGCT	GGGGTGGCTC	1800
AGCCAAACCT	TGAGCCCTAG	AGCCCCCTC	AACTCTGTTC	TCCCCTAGGG	GCTCCCTGGT	1860
GTTGGCCTCA	CACCTTCAGC	TGCCCAGACT	GCCCGTCAGC	ACCCCAAGAT	GCATCTTGCC	1920
CACAGCACCC	TCAAACCTGC	TGCTCACCTC	ATTGGTAAAC	ATCCACCTGA	CCTCCCAGAC	1980
ATGTCCCCAC	CAGCTCT					1997

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10240 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GAATTCCCCG	GATCAAAGTC	AGCATTAAAT	CCCAGTTTAG	GTTTTGAGGC	TAAGTTCAAG	60
TTTGAGTCTA	ATGTCATTTT	AGCCTTGTTT	GGAGGACTCA	GAGATTTTAC	TAGTTTCTCC	120
GCAGAGACCA	CTGTAGAAAC	TGCATTTCCC	TGAGTTTTGG	GCACAAGACT	CCAGTCATCA	180
CCCCTCCCCA	ACAGGGAAAG	CCCCAAACCA	ACTGCTGGCC	TCCTCAAGAA	AGAAACCGAA	240
TTTCACACAA	CCTCCGAAAC	TAAGATTGAA	ACCAAGATTG	GCCCATCTCA	AGGCGCGTCC	300
TCCAGCACAT	TGAGAATGTC	GCTGATGGAG	CCTCGGCCCA	GCTCTCGAGC	TTCCCTTCCTT	360
TCTGTCTCTC	ATGTCCTTCT	ATCACTCCCT	CTCACCTTCC	CGTTTTTGTG	CTGCAATGCC	420
CCCTTCTTCC	TCTCTTCCTG	GGGTTTTTTCC	CTTTATTTCT	CACTGTACCA	TTTTTATATTT	480
TAATAAAGCC	GAGGTCTCCT	AGTCCATCAG	CTCCTACTGT	TGGAGAGGAG	GCAGAAAGAA	540
ACAGCAGGAC	GGCAAAGGGA	CTCCAGAGAA	AGAGACTCAG	AGGAAAGGCA	AGAAACAGGG	600
ACCAAGAGAG	AGGCCAACAG	TGACACAAGA	CACAGTGAGG	TTAAAGAGAA	TAAGATGAGG	660
CCAAGATAGA	GACCAAGCTA	TTTAAAGAG	CCATCTGTGG	CTACCCCTCT	TCCGCCATCG	720
CATCTGGTCA	GCCACCAAGA	TTTTGCCCTAG	AAACGTTCCCT	CCTCTCCATT	CTCCTGCTGC	780
TGCTGTGCTG	GCTGTGCTG	CTGCTGCTGC	TGCTGCTGCT	GCTGCTGCTG	CTGCCTTAAT	840
ACGAATGCAG	GCTCTTGTC	TCTCCTTGCT	GGGTGTGTC	AAAATCCTCC	TAACTGGTCT	900
CCACACTTCT	CATTTCCCCCT	CCAGCCCCCC	ATCTTCCATA	CTTCCATTTA	TTTATTTTGG	960
CCATGCCCCAT	GGCATGTGGC	AGTTCCAGGG	GCCAGGGATC	AAACCTGTGC	CAATGCAGTG	1020
ACCGTGTCTAG	ATCCTTAACC	CACTGCACAC	AAGGCAACGC	CCCTCGAGTC	ATTCTCATTT	1080
TTTAAATATA	CCAATTTGAG	GGGGTCCCTC	TTTCACTTAA	AAATTTTGGC	AGCTCCCTAT	1140
CATGATGAGA	AGGAATTCCA	AACCATTTTT	CTTGTGTGCA	AACCCCTCAG	CATGTGTCCT	1200
CAGCTTACTT	CCCAAGCCTC	ATCCCTGCTC	CTTCTACGTG	TACCCATGTG	TACATCTCCA	1260
CACACCATAT	ACTCTTTTTT	ACCTCCCATC	TTTGACCTT	CTGTTCCCTC	TCTCTGCCCC	1320
TCACCATCTT	TTTTTGCTTT	ATACTTAATG	CCTCTCCCTC	AGGCCAGGTT	CAATGGCTTT	1380
TCTGTGGGCT	GCTTTAAGCC	CACGTGTCATG	GAACTTATCA	CATTTTATTT	TATTTGACTT	1440
TCTTTTTAGG	GCCGCACCCA	GCATATGGAG	ATTCCCAGGC	TAGGGATCTA	ATCGGAGCTG	1500
TATCTGCCAG	CCTGCGCTGG	AGCCACAGCA	ACGTGGGATC	CGAGCCTGAG	GGGTTTTGAT	1560
GTCTGTGGC	ACAGAAGTTA	CATTCAGGCT	GTGCATGAAC	TATTTCTCCT	GTTCTCCTCC	1620
CCCTGCTTGA	GGCCCTGCAG	CTTTGCCCTC	CATGCCCTGC	TGCTCTGACC	TATGACTTCT	1680
TTTTGTTTGC	ATTCCATCTC	TTTAGTTTTT	TCTCTGTTCC	ACAAACATTT	ACTGAGCATC	1740
TACATGAGGC	ATTGAGGATA	CGGATGGGAA	AGACAGTCCC	CTGACCTCTG	GGACCTCAAA	1800
GACCAATTGT	GGAAGACTGG	TTGGTTATCA	GATAATTACA	ATGAAGTGTG	GGAGTCCCTG	1860

TCATGGGTCA	GCAGGTAATG	AACCCAGTAA	ACGATCCATG	AGGATGCAGA	TTCAATCCCT	1920
GGCCTTGCTC	AGCGGGTTAA	GGATCCAGCG	TTCCCACAAG	CTGTGGTGTA	GGTCGCAGAT	1980
GCGACTCAGA	TCTTGCAATTG	CTGTGGCTGT	GGTGTAGGCT	GGTGGCTACC	CCTAGCCTGG	2040
GAACCTCCAT	ATGCCTCAGG	TGCGGCCCTA	AAAGACAAAA	AAAAAAAAGA	GAGAAACTTT	2100
TCTTTTCTT	AATGTGTAAC	CTACAAGCTA	AGTGAAAACT	GGCTCCTATT	CCATAACGTT	2160
TGTATCATTT	TTCATACTAG	CCAAATACTA	GAAACAGGGA	GTTCCCGTCG	TGGTGCAGCA	2220
GAAACAAATT	CGACTAGGAA	CCATGAGGTT	GCGGGTTCGA	TCCCTGGCCT	TGCTCAGTGG	2280
GTTAAGGATC	CGGCGTTGCC	GTGAGCTGTG	GTGTAGGTCG	CAGATGTGGC	TCGGATCTAG	2340
TGTTGCTGTG	GCTCTGGTGT	AGGCCGGCAG	CAACAGCTCT	GATTAGACTC	CTAGCCTGAG	2400
AACCTCCATA	AGCTGTGGCT	GCGGCCCTAT	AAAGACAAAA	AAAAAAAAAA	GGCCAAATAC	2460
TAGAAACAAA	CCAAATGCCC	ATCAACAGAA	GAATAGATAA	GTTAATTGGG	GTATATGCAC	2520
ACAATAGCAT	CACACAATAA	CATGCACACA	ATAACATCAC	AATGAAATAA	AAATTACTAC	2580
TGACAGACAC	AACCATATAG	ATGAATTTCA	CAAACACAAC	AGCGAGAATA	AAAGCCAAGC	2640
ACAGATGAGT	TGTCTGTGTG	GATTCATTTT	TATGAAGTTC	AAGCGCAGGA	AGAACTTAAT	2700
CTATAGTGAC	AGAGGTGAGA	GAGCAGTTGG	TTGTCTTTGG	CAGGTATGAA	CTGGGAGTGG	2760
GCATGAGAGA	ACTTTCTGGA	GACCTAAAAA	TATATTGGAC	TGGATGGTGG	CAACATGGCT	2820
ACAAGAAGAT	GGAAAAGTTC	CTCAGGCTGT	CCACTTGGGA	GACGGGCTTC	TCACGGGACC	2880
TAAGTTCTGC	ATCAGCAGAG	GGGGAAATCC	TTAATGATTT	GACAATTACA	AAGTGTATTG	2940
GCTTTACCGA	TGTATTTTCA	ACACAATCCC	TCTGCTGTCC	CCACCCACC	CTAGGTCACC	3000
ACCTTTAAGC	TCCACCTGTG	TGGAATTTCTG	AAGCCTCCCC	TGTAGAGAAC	TTTAGCAGTT	3060
GCCACGTTCT	TTTGATGCAG	GAACGTGTTG	TCTAGAGTTA	GACACATCTG	ATCTGTGGGG	3120
CCCACCCAAG	GTTGGGACAT	GGTGGGGGGC	GGCCTTCTGC	AGTGAGATGA	AACCTCATTTG	3180
TAGGTGATTT	CGTGGCCTCA	TCCCTGAGTC	AGATCTTCCA	AATGAGGACA	CTTTGGAGAG	3240
CAAAGGGGG	CTCCCTGAAG	ATTTCTCTCA	GGACAGCAGG	AACAAACCAG	GATGTCCCAG	3300
GCAGGAGGGT	ATAGAAGGGA	ACTTGTGTGAT	ATGAAATCAG	CCAGATGACC	TGGAAAATAC	3360
ACAGACTGGG	ACAAGTGTGA	CTTGAGCCTC	TTGGGCCCCAG	GACAGGGGTA	CAGAGGAGGA	3420
AACGTGCACA	GAGAGAAAGC	CGTAATCAGC	CAAGGCTGCA	GAGGTGTTAT	ACATAATCGC	3480
TCTTCACGCA	ACCGGGCAAG	CAGCCCACGC	CCCAGCTGCA	CTCCATCTCC	TCCTCTGAAC	3540
TCACCGTCCC	TTCTCTGGAA	CTCCTAAGCC	TGACCCCGCT	CCCTGGCCCT	CCCAGCCCAC	3600
GGTTCCCCTG	ACCCCACTCC	CTTTCCCAGA	ACTCAGTCAT	CTGAGCCCCC	AGCCTGCGTT	3660
CTCTCCTAGG	CCTCAGCCTT	TCCTGCCTTC	GCGTGAAACA	GCAGCATCTT	CTAAGCCCTG	3720
GGCTTCCCCA	GGCCCCAGCC	CCGGCCTAGA	ACCCGCCCAG	CCGACCTGCC	CACGCTGCCA	3780
CTGCCGGCTT	CCTCTATAAA	GGGACCCAGG	GCGCCAGAA	AGGGGCCCC	AGGGGTCCCC	3840
CACAGCAGGT	GAGACTCTCC	CACCCCATCT	CCTAGGGCTG	TCCGGGTGCT	GGACTCCCCC	3900
CTCACTTCGG	TCCCTCCGCC	CGCTCCCTGG	CCTTCTCTGCC	CCTCCTGCAT	CTTCACCCCG	3960
GCCTGGGCCCT	TGGTGGGTTT	GGTTTTGGTT	TGTTCTCTCT	GATTCTTTAT	CTGTCAGGCT	4020
CTTTCTAGCT	CTCACACACT	CTGATCCCTC	TCTGTTCCCT	TCCCATCTCT	GTTTCTCTCT	4080
GGGTCTCCCC	CTGCTCACCT	CGGGATTTCC	CTGAGTGCCT	CTGGTCCCCT	TCTCTGTCTG	4140
GCGCCCCGTC	TCTTGTCTCT	CGGGGTGGCT	GTCTCCGAGG	GCAGGAGGCC	TTCTTCCGCA	4200
GGTGCCCCGC	CCCGCTCACT	GTCTCTCTCC	CCCCACAGGT	TTTCCCCATG	ACACCACCTG	4260
GACGCCCTTA	CCTCCGGAGG	GTGTGCAGCA	CCCCCATCCT	CCTCCTCCTG	GGGCTGCTGC	4320
TGGCCCTGCC	GCCCGAGGCC	CAGGTGAGGC	AGCAGGAGAG	CGGGCCGTGG	GGGCAGCCTT	4380
CGCCAACCTT	GGGCTCAGA	GCCTCTCTGA	CGCTCTTCTC	CCCTAGGGGC	TCCCTGGCGT	4440
CGGCCTCCCA	CCCTCAGCTG	CACAGCCTGC	CCATCAGCAC	CCCCCAAAGC	ACTTGGCCAG	4500
AGGCACCCCT	AAACCTGCCG	CTCACCTCGT	TGGTAAACAT	CCACCTGGCC	TCCCAGACCT	4560
GTAGCCCCCA	GTCTCTCTCC	TATGCCCTTG	CTTCAGGGAC	TGAAGCATCC	CTCCCCCCCC	4620
TCTCCCCCCA	CCCCCTAAAT	GGAGGCATCC	CACTCCCGAC	TCCCTCCCCA	CCATCCCCCA	4680
GGAACTCAGT	CCAGCACCTG	CTTCCCTCAGG	GATTGAGACC	TCCGACCCCC	AGGTCTTTGA	4740
CTCCCACCCC	CTCTGGCTCT	TCCTAGGAGA	CCCCAGCACC	CCGGACTCAC	TGCGCTGGAG	4800
AGCGAACACG	GATCGTGCCT	TCCTCCGCCA	TGGCTTCTTG	CTGAGCAACA	ACTCCCTGCT	4860
GGTCCCCACC	AGTGGCCTCT	ACTTTGTCTA	CTCCCAGGTC	GTCTTCTCCG	GGGAAGGCTG	4920
CTTCCCCAAG	GCCACCCCA	CCCCTCTCTA	CCTGGCCAC	GAGGTCCAGC	TCTTCTCCTC	4980
CCAGTACCCC	TTCCACGTGC	CGCTCCTCAG	CGCTCAGAAG	TCCGTGTGCC	CCGGGCCACA	5040
GGGACCTTGG	GTGCGCTCTG	TGTACCAGGG	GGCTGTGTTT	CTGCTCACCC	AGGGAGATCA	5100
GCTGTCCACA	CACACAGACG	GCACCCCCCA	CCTGCTCCTC	AGCCCCAGTA	GCGTCTTCTT	5160
TGGAGCCTTC	GCTCTATAGA	AGAATCCAGA	AAGAAAAAAA	TTGGTTTCAA	GGCCTTCTCC	5220
CCTTTTACC	TCCCTTATGA	CCACTTCGGA	GGTCACCGCG	CCTCTCCTCT	GACAATTTCC	5280
AACAGTCTCA	TCTTCCCCCA	CGCTCAGCAC	CTGGAGCTTC	TGTAGAAGGA	ATTCTAGGCA	5340
CCTCGGGGGA	ACTGGAACCA	CCCCGGATGC	TCTGCTGAGG	ATCTGAATGC	CCGCCTGGAG	5400
CCCTTCCCCCT	GTCTTGCCCC	TCTAGGGGCC	CTCGTCCAGG	ACGTGGAAGG	GAAGCTGACC	5460

CATGAGGGAC	TTTGAACGGA	TGACCGGAGC	GGTGTGGGGG	GGTTATTTAT	GAAGGGGAAA	5520
ATTAAATTAT	TTATTTATGG	AGGATGGAGA	GAAGGGAATC	ACAGAGGGAT	GTCAGAAGAG	5580
TGTGACACAT	GTGCCAAGA	GATAAAGTGA	CAGAAGGCAT	GGGCTCCAGA	TGACCCGGCC	5640
AGAGAGGGCA	AAGTGGCTCA	GGGAGGGGCT	GCTTGACTGG	AGGCTCATGA	GGAGACGGCT	5700
GACCCTCGAT	GAAACCCAAT	AAAAGCTCTTT	TCTCTGAAAT	GCTGTCTGCT	CGTATCTGTC	5760
ACTCGGGAGG	GGAGAATTCT	CCAGATGTCT	CTAAGGAGTG	GAGGGAGGAC	AGGAATCAGA	5820
GGGGACGGGA	GCTGTGGGTG	TGTGATGAGG	CCTAAGGGGC	TCAGGTGAGA	GATGGCGGCC	5880
TCAGGGTGAG	GGCAGCCAGA	CCCCTGCAGG	AGAAGCAGAT	GGTTCCTCTG	AGAAGACAAA	5940
GGAAAGAGATG	CAGGGCCAAAG	GCTCTGAGAA	CCGAGGTCGG	GGGTGCGCTG	CAGAGATATGG	6000
CCACAGGTAG	AGGGACAGAG	GAATAGGGGT	GACAGGAGGC	TTCCCGGGAG	AAGGGAACAC	6060
ACTGAGGGGT	GTTCTGGGAT	CTGAGGGAGG	AGCACGGGGA	CGCCCTGGGA	GACATGCCGT	6120
CCAGGGCCAT	GAGGAGTGGG	AGAGCCTCTG	AGGCTAGCGG	CTGGAGATAC	AGGGACATTT	6180
GAGGAGACAC	GGTCATGGCC	AGGAGCCGCG	AGGGCCTGGA	CAGTCTCTAG	GAATCTCGAA	6240
GAAGCAGGAA	TTCTTTGAGG	ATACGTGGCC	ACACAAAGGG	AGGCTGAGGT	GTGGGGACTT	6300
CATGCAGAAG	TCAGGGCCTC	ACATTCCCTT	GGAAGCCGAG	ACTGAAACCA	GCAGCAGAGT	6360
TTTGGTGAGT	TCCTGTCAGA	GTGAAAGGAG	AAGGCCCGCC	ATGGTGGGTT	TGTGAATTCC	6420
CAGCCTGGCT	TCCCTGTCCT	CTGGGGCTGT	CCGAGCCCTG	TTCTGTCCGT	CCTCCCCCAG	6480
CCCGTGTAGG	GCCTCCAGCT	GCCCTTCTCC	CAGTCTCTCT	TCCCTCCAGG	AGACGAAACA	6540
TGGGTCTCAG	CACCCAGCGC	GGTGTCTGCT	AAGTTTTCTC	TCCATTAAGA	ACTCAGCTTT	6600
CTGAAGCTCC	TCCCATTCTT	AGTTCTACCC	CTACCTGAGC	CCTGTTCTGGA	AATCAGAGAG	6660
AAATAGAAGT	CATCCCCCAA	AGAAAAGGAA	TTTGTCCCCC	AAAGAAACAG	AACTTGTCCC	6720
CCAAAGAAAT	GGAAACAATG	GGAAATGGGA	GGCAGGGGGG	ACCTGGGGTC	CAGCCTCCAG	6780
GGTCTTACAC	ACAGAGCAGT	AACTGGCCCA	GCAAGCCCAT	CTCAGGATCC	GGGCAGGGAG	6840
GGTAGGAAGT	ATCCCTGATG	CCTGGGTGTC	CCCACTTTTC	CAAACCGCCG	CCCCGCCTAT	6900
GGAGATGAAA	CTAAGACAGA	AGGTGCAGGG	CCCGCTACCG	CTTCTCTCCG	ATGAGCTCAT	6960
GGGTTTCTCC	ACCAAGGAAG	TTTTCCGCTG	GTTGAAAGAG	AGCCTCTCCC	CGCCCTCTTC	7020
TCACCCAGAG	CGTATAAATG	CAGCTGTTTG	CACACCCAGC	CAGCAGAAGC	TCCAGAGGTG	7080
AGGACACCAG	GGGACCAGCC	AGGAGAGAGA	CAAGCCATCT	CCAGGACCCC	CTAGAAATAA	7140
CCTCTCAGAA	GACACACCCC	CGAACAGGCA	GCCGGACGAC	TCTCTCCCTC	TCACACGCTG	7200
CCCCGGGGCG	CCACCATCTC	CCAGCTGGAC	CTGAGCCCCC	CTGAAAAAGA	CACCATGAGC	7260
ACTGAGAGCA	TGATCCGAGA	CGTGAGAGTG	GCGGAGGAGG	CGCTCGCCAA	GAAGGCCGGG	7320
GGCCCCCAGG	GCTCCAGGAG	GTGCCTGTGC	CTCAGCCTCT	TCTCCTTCCT	CCTGGTTCGA	7380
GGAGCCACCA	CGCTCTTCTG	CCTACTGCAC	TTCCAGGTTA	TCGGCCCCCA	GAAGGAAGAG	7440
TGTAGCGCCT	GGCCAGCCCT	GGCTCATTTCT	CCCAGCCGGA	GAGAAATGGG	GAAGAAAGAG	7500
GGCCAGAGAC	GAGCTGGGGG	AAAGAAGTGT	GCTGATGGGG	AGTGTGGGGA	GGAAATCATG	7560
GAGAAAGATG	GGGAGGCAGA	AGGAGACGTG	GAGAGAGATG	GGGGGAGAGA	GAGAAGGATG	7620
GAGAGAAATC	CGGTGGCCCG	GCCCTTGGA	ATGCTCTCTA	AATATTTGTT	GCACGAATGA	7680
GTGAGTAAGC	AGGGACACCG	ATATAAAGAG	AGATGAGTAG	ACAGACAAGG	GGTGTGGTAG	7740
AAAGATAGGG	AAAAACAAG	TGATCTGGAT	AAAGATAGTG	AGACAGGAAG	AGGTAGAGGA	7800
GATAGGAAAG	AGAGATAAGG	AGAGAAGAAG	GAAGCGTG	TGTCTGGCAC	GTGGAAGGCA	7860
CTCAATGAAG	GAGTTGTTGA	ATGGATGGGT	GGATGAGAAA	ATGGATGAGT	GGAGAGAAAA	7920
AACTAGACAT	CAGGGCAGAG	AGGTACAAGCT	AGAGAAGCAG	GTGGCTGTTT	TCCCTTCAGA	7980
GGGGACTTAT	TCAAATCTAA	TTAATCCTTC	TTCTTCTCCC	CAACAGTTTC	CAGCTGGCCC	8040
CTTGAGCATC	AACCTCTTGG	CCCAAGGACT	CAGTAAGTAT	CTCTAAAACC	TGTCTCTCAG	8100
TTCTGAGCTT	GGACAGGGGT	GGGGTTAGTG	CTGGGGTGGA	AGGAAGAAGG	GAAATTTAGG	8160
GTCTGGGTTT	GGCGGGGGGA	ATGCAGGTCA	AAGTAGTGAG	ATATTTTCTG	GGAAGTCTGA	8220
GGGTCTCATC	TTTTTCTTTC	CTCTTCTCTC	CTCAGGATCA	TCGTCTCAAA	CCTCAGATAA	8280
GCCCGTCGCC	CACGTTGTAG	GTAAGAGTTC	TGAGGATGTG	TCTGGGGGAT	GAAGAAATAG	8340
GCAGGACAGA	GAGGGATAGG	ATTTGGGGGC	TGAAGCCAGG	CTGAGGGGAT	CCAGAGCTTG	8400
GAGATAGTAT	GAGGAGGACT	CGTGTAGCTC	CAGGGGAGGA	TGGGGGATAC	TCAGAGACTTG	8460
AGGAGGATAC	TCGGAACCTC	ATGGACAGAT	GGGATGTGGG	AAGACAGACC	GAGGGGACAG	8520
GAACCGGATG	TGGGGGGCGG	GCAGAACTCG	AGGGCCAGGA	TGTGGAGAGT	GGAAGTACAC	8580
GGGTACACT	GACTCACCCC	TCCCTCTTTG	TCTCTCTCCT	CCAGCCAATG	TCAAAGCCGA	8640
GGGACAGCTC	CAATGGCAGA	GTGGGTATGC	CAATGCCCTC	CTGGCCAACG	GCGTGAAGCT	8700
GAAAGACAAC	CAGCTGGTGG	TGCCGACAGA	TGGGCTGTAC	CTCATCTACT	CCCAGGTCTT	8760
CTTCAGGGGC	CAAGGCTGCC	CTTCCACCAA	CGTTTTCTCT	ACTCACACCA	TCAGCCGCAT	8

[illegible]

CGTTCCCTCC	CCTGTCCATC	CCTTTATTAT	TTTACTCCTT	CAGACCCCCCT	CACGTCCCTC	9120
TGGTTTAGAA	AGAGAATGAG	GGGCTGGGGA	CTGGGCTCCA	AGCTTAAAAC	TTTAAACAAC	9180
AACAGCAACA	CTTAGAAATC	AGGGATTGAG	GGATGTGTGG	CCTGGACAAC	CAGGCACTGA	9240
CCACCACCAA	GAATTGGAAC	TGGGGCTTCC	AGACTCGCTG	GGGTCCCTGG	GTTTGGATTG	9300
CTGGATGCAA	CCTGGGACAT	CTGGAATGTG	GCTGCCAGGG	AAGCTTGGGT	TCCAATCGGA	9360
ATACTTCAGA	ACATTCCCTG	AGAAGATTTT	ACCTCAATCT	TGATGACTTT	TTAGGCTTCC	9420
CTTTCTTCCA	ATTTTCCAGA	CTTCCCTGGG	ATGGGGAGCC	CAGCCCCAAA	CCCCACAGGC	9480
CAGCTCCCTC	TTATTTATAT	TTGCACTTGG	CATTATTATT	TATTTATTTA	TTTATTATTT	9540
ATTTACTAGT	GAATGTATTT	ATTGAGGAGG	GCGAGGTGTC	CTGGGAGACC	CAGCATAAGG	9600
GCTGCCTTGG	TTCAGATGTG	TTTTCTGTGA	AAACGGAGCT	GAAGTGTAGG	TTGCTCCAC	9660
CTGGCCTCCT	AGCCTCTGTG	CCTCCTTTTG	CTTATGTTTT	TAAAAACAAA	TATTTATCTG	9720
ATCGAGTTGT	CTAAATAATG	CTGATTTGGT	GAATAACTTG	TCGCTACATC	GCTGAACCTC	9780
TGCTCCCCAG	GGGAGTTGTG	TCTGTAACCG	CCCTACTGGT	CAGTGGCGAG	AAATAAAAGC	9840
GTGCTTAGAA	AAGAAATCTG	GCCTCTTTCT	GCGACTGAAT	TCTGCATCTC	CTTGGGGGGG	9900
TGAGGCTGCT	CCCCAAAAT	CTTCTCCAC	CGGGCTTAGG	ATTCCCTGGG	CTTCACTCCT	9960
GAGCTTGGAC	TGCCTGGCTC	AGGAGCCTCT	GCAAGAAACA	AAGCCCAGCC	AAACAGGTCC	10020
CTCCCCTAAG	AAAGGAACCT	GAAGGTAATT	ACCTCTCCCT	CAGGGTGTGG	GAATTTCCAA	10080
GTCTGGGAAT	TCCTATCCAG	CTGGGGAAGT	CTGCAGTGCA	GGTGAGACTT	CCGGCTGAAA	10140
GAGCCAGGGA	GCGGCCAGAT	GCTCAGGTAC	CTGAACCAGA	GCCAAGGGAC	TTCCAGACAG	10200
TGAGGCAACT	GGGCTCCAAA	TAACCTGATC	CGGGGAATTC			10240

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1644 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CCTCAGCGAG	GACAGCAAGG	GACTAGCCAG	GAGGGAGAAC	AGAAACTCCA	GAACATCCTG	60
GAAATAGCTC	CCAGAAAAGC	AAGCAGCCAA	CCAGGCAGGT	TCTGTCCCTT	TCACTCACTG	120
GCCCAAGGCG	CCACATCTCC	CTCCAGAAAA	GACACCATGA	GCACAGAAAG	CATGATCCGC	180
GACGTGGAAC	TGGCAGAAGA	GGCACTCCCC	CAAAAGATGG	GGGGCTTCCA	GAAGTCCAGG	240
CGGTGCCTAT	GTCTCAGCCT	CTTCTCATTC	CTGCTTGTGG	CAGGGGCCAC	CACGCTCTTC	300
TGTCTACTGA	ACTTCGGGGT	GATCGGTCCC	CAAAGGGATG	AGAAGTTCCC	AAATGGCCTC	360
CCTCTCATCA	GTTCTATGGC	CCAGACCCCT	ACACTCAGAT	CATCTTCTCA	AAATTCGAGT	420
GACAAGCCTG	TAGCCACAGT	CGTAGCAAAC	CACCAAGTGG	AGGAGCAGCT	GGAGTGGCTG	480
AGCCAGCGCG	CCAACGCCCT	CCTGGCCAAC	GGCATGGATC	TCAAAGACAA	CCAAGTAGTG	540
GTGCCAGCCG	ATGGGTTGTA	CCTTGTCTAC	TCCCAGGTTC	TCTTCAAGGG	ACAAGGCTGC	600
CCCGACTACG	TGCTCCTCAC	CCACACCGTC	AGCCGATTTG	CTATCTCATA	CCAGGAGAAA	660
GTCAACCTCC	TCTCTGCCGT	CAAGAGCCCC	TGCCCCAAGG	ACACCCCTGA	GGGGGCTGAG	720
CTCAAACCTC	GGTATGAGCC	CATATACCTG	GGAGGAGTCT	TCCAGCTGGA	GAAGGGGGAC	780
CAACTCAGCG	CTGAGGTCAA	TCTGCCCAAG	TACTTAGACT	TTGCGGAGTC	CGGGCAGGTC	840
TACTTTGGAG	TCATTGCTCT	GTGAAGGGAA	TGGGTGTTCA	TCCATTCTCT	ACCCAGCCCC	900
CACTCTGACC	CCTTTACTCT	GACCCCTTTA	TTGTCTACTC	CTCAGAGCCC	CCAGTCTGTG	960
TCCTTCTAAC	TTAGAAAAGG	GATTATGGCT	CAGAGTCCAA	CTCTGTGCTC	AGAGCTTTCA	1020
ACAACACTCT	AGAAACACAA	GATGCTGGGA	CAGTGACCTG	GACTGTGGGC	CTCTCATGCA	1080
CCACCATCAA	GGACTCAAAT	GGGCTTTCCG	AATTCACCTG	AGCCTCGAAT	GTCCATTCTT	1140
GAGTTCCTGA	AAGGGAGAGT	GGTCAGGTTG	CCTCTGTCTC	AGAATGAGGC	TGGATAAGAT	1200
CTCAGGCCTT	CCTACCTTCA	GACCTTTCCA	GACTCTTCCC	TGAGGTGCAA	TGCACAGCCT	1260
TCCTCACAGA	GCCAGCCCCC	CTCTATTTAT	ATTTGCACTT	ATTATTTATT	ATTTATTTAT	1320
TATTTATTTA	TTTGCTTATG	AATGTATTTA	TTTGGAAGGC	CGGGGTGTCC	TGGAGGACCC	1380
AGTGTGGGAA	GCTGTCTTCA	GACAGACATG	TTTTCTGTGA	AAACGGAGCT	GAGCTGTCCC	1440
CACCTGGCCT	CTCTACCTTG	TTGCCTCCTC	TTTTGCTTAT	GTTTAAAACA	AAATATTTAT	1500
CTAACCCAAT	TGTCTTAATA	ACGCTGATTT	GGTGACCAGG	CTGTCGCTAC	ATCACTGAAC	1560

CTCTGCTCCC	CACGGGAGCC	GTGACTGTAA	TTGCCCTACA	GTCAATTGAG	AGAAATAAAG	1620
ATCGCTTAAA	ATAAAAAACC	CCCC				1644

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	1890 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single
(D)	TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

AAACAGAGAG	AGATAGAGAA	AGAGAAAGAC	AGAGGTGTTT	CCCTTAGCTA	TGGAAACTCT	60
ATAAGAGAGA	TCCAGCTTGC	CTCCTCTTGA	GCAGTCAGCA	ACAGGGTCCC	GTCTTGGACA	120
CCTCAGCCTC	TACAGGACTG	AGAAGAAGTA	AAACCGTTTG	CTGGGGCTGG	CCTGACTCAC	180
CAGCTGCCAT	GCAGCAGCCC	TTCAATTACC	CATATCCCCA	GATCTACTGG	GTGGACAGCA	240
GTGCCAGCTC	TCCCTGGGGC	CCTCCAGGCA	CAGTTCTTCC	CTGTCCAACC	TCTGTGCCCCA	300
GAAGGCCTGG	TCAAAGGAGG	CCACCACCAC	CACCGCCACC	GCCACCACTA	CCACCTCCGC	360
CGCCGCCGCC	ACCACTGCCT	CCACTACCGC	TGCCACCCCT	GAAGAAGAGA	GGGAACCACA	420
GCACAGGCCT	GTGTCTCCTT	GTGATGTTTT	TCATGGTTCT	GGTTGCCTTG	GTAGGATTGG	480
GCCTGGGGAT	GTTTCAGCTC	TTCCACCTAC	AGAAGGAGCT	GGCAGAACTC	CGAGAGTCTA	540
CCAGCCAGAT	GCACACAGCA	TCATCTTTGG	AGAAGCAAAT	AGGCCACCCC	AGTCCACCCC	600
CTGAAAAAAA	GGAGCTGAGG	AAAGTGGCCC	ATTTAACAGG	CAAGTCCAAC	TCAAGGTCCA	660
TGCCCTCTGA	ATGGGAAGAC	ACCTATGGAA	TTGTCTTGCT	TTCTGGAGTG	AAGTATAAGA	720
AGGGTGGCCT	TGTGATCAAT	GAACTGGGC	TGTACTTTGT	ATATTCCAAA	GTATACTTCC	780
GGGGTCAAATC	TTGCAACAAC	CTGCCCCTGA	GCCACAAGGT	CTACATGAGG	AACTCTAAGT	840
ATCCCCAGGA	TCTGGTGATG	ATGGAGGGGA	AGATGATGAG	CTACTGCACT	ACTGGGCAGA	900
TGTGGGGCCCG	CAGCAGCTAC	CTGGGGGCAG	TGTTCAATCT	TACCAGTGCT	GATCATTTAT	960
ATGTCAACGT	ATCTGAGCTC	TCTCTGGTCA	ATTTTGAGGA	ATCTCAGACG	TTTTTCGGCT	1020
TATATAAGCT	CTAAGAGAAG	CACTTTGGGA	TTCTTTCCAT	TATGATTCTT	TGTTACAGGC	1080
ACCGAGAATG	TTGTATTTCAG	TGAGGTCCTT	CTTACATGCA	TTTGAGGTCA	AGTAAGAAGA	1140
CATGAACCAA	GTGGACCTTG	AGACCACAGG	GTTCAAAATG	TCTGTAGCTC	CTCAACTCAC	1200
CTAATGTTTA	TGAGCCAGAC	AAATGGAGGA	ATATGACGGA	AGAACATAGA	ACTCTGGGCT	1260
GCCATGTGAA	GAGGGAGAAG	CATGAAAAAG	CAGCTACCCA	GGTGTTCCTAC	ACTCATCTTA	1320
GTGCCTGAGA	GTATTTAGGC	AGATTGAAAA	GGACACCTTT	TAACCTCACCT	CTCAAGGTGG	1380
GCCTTGCTAC	CTCAAGGGGG	ACTGTCCTTC	AGATACATGG	TTGTGACCTG	AGGATTTAAG	1440
GGATGGAAAA	GGAAGACTAG	AGGCTTGTCAT	AATAAGCTAA	AGAGGCTGAA	AGAGGCCAAT	1500
GCCCCACTGG	CAGCATCTTC	ACTTCTAAAT	GCATATCCTG	AGCCATCGGT	GAAACTAACA	1560
GATAAGCAAG	AGAGATGTTT	TGGGGACTCA	TTTCATTCCCT	AACACAGCAT	GTGTATTTCC	1620
AGTGCCAATT	GTAGGGGTGT	GTGTGTGTGT	GTGTGTGTGT	GTGTATGACT	AAAGAGAGAA	1680
TGTAGATATT	GTGAAGTACA	TATTAGGAAA	ATATGGGTTG	CATTTGGTCA	AGATTTTGAA	1740
TGCTTCCTGA	CAATCAACTC	TAATAGTGCT	TAAAAATCAT	TGATTGTCAG	CTACTAATGA	1800
TGTTTTCCCTA	TAATATAATA	AATATTTATG	TAGATGTGCA	TTTTTGTGAA	ATGAAAACAT	1860
GTAATAAAAA	GTATATGTTA	GGATACAAAT				1890

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	1541 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single
(D)	TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

GGGTGTCTCA	CAGAGAAGCA	AAGAGAAGAG	AACAGGAGAA	ATGGTGTTTC	CCTTGACTGC	60
GGAACTTTA	TAAAGAAAAC	TTAGCTTCTC	TGGAGCAGTC	AGCGTCAGAG	TTCTGTCCTT	120
GACACCTGAG	TCTCCTCCAC	AAGGCTGTGA	GAAGGAAACC	CTTTCCCTGGG	GCTGGGTGCC	180
ATGCAGCAGC	CCATGAATTA	CCCATGTCCC	CAGATCTTCT	GGGTAGACAG	CAGTGCCACT	240
TCATCTTGGG	CTCCTCCAGG	GTCAGTTTTT	CCCTGTCCAT	CTTGTGGGCC	TAGAGGGCCG	300
GACCAAAGGA	GACCGCCACC	TCCACCACCA	CCTGTGTCAC	CACTACCACC	GCCATCACAA	360
CCACTCCCAC	TGCCGCCACT	GACCCCTCTA	AAGAAGAAGG	ACCACAACAC	AAATCTGTGG	420
CTACCGGTGG	TATTTTTCAT	GGTTCTGGTG	GCTCTGGTTG	GAATGGGATT	AGGAATGTAT	480
CAGCTCTTCC	ACCTGCAGAA	GGAAGTGGCA	GAAGTCCGTG	AGTTCACCAA	CCAAAGCCTT	540
AAAGTATCAT	CTTTTGAAAA	GCAAATAGCC	AACCCAGTA	CACCCCTCTGA	AAAAAAAGAG	600
CCGAGGAGTG	TGGCCCATTT	AACAGGGAAC	CCCCACTCAA	GGTCCATCCC	TCTGGAATGG	660
GAAGACACAT	ATGGAACCGC	TCTGATCTCT	GGAGTGAAGT	ATAAGAAAGG	TGGCCTTGTG	720
ATCAACGAAA	CTGGGTTGTA	CTTCGTGTAT	TCCAAAGTAT	ACTTCCGGGG	TCAGTCTTGC	780
AACAACCAGC	CCCTAAACCA	CAAGGTCTAT	ATGAGGAACT	CTAAGTATCC	TGAGGATCTG	840
GTGCTAATGG	AGGAGAAGAG	GTTGAACTAC	TGCACTACTG	GCCAGATATG	GGCCACACAGC	900
AGCTACCTGG	GGGCAGTATT	CAATCTTACC	AGTGCTGACC	ATTTATATGT	CAACATATCT	960
CAACTCTCTC	TGATCAATTT	TGAGGAATCT	AAGACCTTTT	TCGGCTTGTA	TAAGCTTTAA	1020
AAGAAAAAGC	ATTTTAAAT	GATCTACTAT	TCTTTATCAT	GGGCACCAGG	AATATTGTCT	1080
TGAATGAGAG	TCTTCTTAAG	ACCTATTGAG	ATTAATTAAG	ACTACATGAG	CCACAAAGAC	1140
CTCATGACCG	CAAGGTCCAA	CAGGTCAGCT	ATCCTTCATT	TTCTCGAGGT	CCATGGAGTG	1200
GTCCTTAATG	CCTGCATCAT	GAGCCAGATG	GAAGGAGGTC	TGTGACTGAG	GGACATAAAG	1260
CTTTGGGCTG	CTGTGTAGCA	ATGCAGAGGC	ACAGAGAAAG	AACTGTCTGA	TGTTAAATGG	1320
CCAAGAGAAAT	TTTAACCATT	GAAGAAGACA	CCTTTACACT	CACCTCCAGG	GTGGGTCTAC	1380
TTACTACCTC	ACAGAGGCCG	TTTTTGAGAC	ATAGTTGTGG	TATGAATATA	CAAGGGTGAG	1440
AAAGGAGGCT	CATTTGACTG	ATAAGCTAGA	GACTGAAAAA	AAGACAGTGT	CTCATTTGCCA	1500
CCATCTTTAC	TGTTACCTGA	TGTTTTCTGA	GCCGACCTTT	G		1541

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 888 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GGCTGGTCCC	CTGACAGGTT	GAAGCAAGTA	GACGCCCAGG	AGCCCCGGGA	GGGGGCTGCA	60
GTTTCCTTCC	TTCCCTTCTC	GCAGCGCTCC	GCGCCCCCAT	CGCCCCCTCT	GCGCTAGCGG	120
AGGTGATCGC	CGCGGCATG	CCGGAGGAGG	GTTTCGGGCTG	CTCGGTGCGG	CGCAGGCCCT	180
ATGGGTGCGT	CCTGCGGGCT	GCTTTGGTCC	CATTGGTTCG	GGGCTTGGTG	ATCTGCCTCG	240
TGGTGTGCAT	CCAGCGCTTC	GCACAGGCTC	AGCAGCAGCT	GCCGCTCGAG	TCACTTGGGT	300
GGGACGTAGC	TGAGCTGCAG	CTGAATCACA	CAGGACCTCA	GCAGGACCCC	AGGCTATACT	360
GGCAGGGGGG	CCCAGCACTG	GGCCGCTCCT	TCCTGCATGG	ACCAGAGCTG	GACAAGGGGC	420
AGCTACGTAT	CCATCGTGAT	GGCATCTACA	TGGTACACAT	CCAGGTGACG	CTGGCCATCT	480
GCTCCTCCAC	GACGGCCTCC	AGGCACCACC	CCACCACCCT	GGCCGTGGGA	ATCTGCTCTC	540
CCGCCCTCCG	TAGCATCAGC	CTGCTGCGTC	TCAGCTTCCA	CCAAGGTTGT	ACCATTGCCT	600
CCCAGCGCCT	GACGCCCCTG	GCCCCGAGGG	ACACACTCTG	CACCAACCTC	ACTGGGACAC	660
TTTTGCCTTC	CCGAAACACT	GATGAGACCT	TCCTTTGGAGT	GCAGTGGGTG	CGCCCCCTGAC	720
CAGTGCTGCT	GATTAGGGTT	TTTTAAATTT	TATTTTATTT	TATTTAAGTT	CAAGAGAAAA	780
AGTGTAACAC	CAGGGGCCAC	CCGGGGTTGG	GGTGGGAGTG	TGGTGGGGGG	TAGTGGTGGC	840
AGGACAAGAG	AAGGCATTGA	GCTTTTCTTT	TCATTTTCCT	ATTAAAAA		888

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1906 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CCAAGTCACA TGATTCAGGA TTCAGGGGGA GAATCCTTCT TGGAACAGAG ATGGGCCCCAG 60
AACTGAATCA GATGAAGAGA GATAAGGTGT GATGTGGGGA AGACTATATA AAGAATGGAC 120
CCAGGGCTGC AGCAAGCACT CAACGGAATG GCCCTCCTG GAGACACAGC CATGCATGTG 180
CCGGCGGGCT CCGTGGCCAG CCACCTGGGG ACCACGAGCC GCAGCTATTT CTATTTGACC 240
ACAGCCACTC TGGCTCTGTG CCTTGCTCTC ACGGTGGCCA CTATTATGGT GTTGGTCGTT 300
CAGAGGACGG ACTCCATTCC CAACTCACCT GACAACGTCC CCCTCAAAGG AGGAAATTGC 360
TCAGAAGACC TCTTATGTAT CCTGAAAAGA GCTCCATTCA AGAAGTCATG GGCCTACCTC 420
CAAGTGGCAA AGCATCTAAA CAAAACCAAG TTGTCTTGGA ACAAAGATGG CATTCTCCAT 480
GGAGTCAGAT ATCAGGATGG GAATCTGGTG ATCCAATTCC CTGGTTTGTA CTTTCATCATT 540
TGCCAACTGC AGTTTCTTGT ACAAAGGCCA AATAATTCTG TCGATCTGAA GTTGGAGCTT 600
CTCATCAACA AGCATATCAA AAAACAGGCC CTGGTGACAG TGTGTGAGTC TGGAAATGCAA 660
ACGAAACACG TATACCAGAA TCTCTCTCAA TTCTTGCTGG ATTACCTGCA GGTCAACACC 720
ACCATATCAG TCAATGTGGA TACATTCCAG TACATAGATA CAAGCACCTT TCCTCTTGAG 780
AATGTGTTGT CCATCTTCTT ATACAGTAAT TCAGACTGAA CAGTTTCTCT TGGCCTTCAG 840
GAAGAAAGCG CCTCTCTACC ATACAGTATT TCATCCCTCC AAACACTTGG GCAAAAAGAA 900
AACTTTAGAC CAAGACAAAC TACACAGGGT ATTAAATAGT ATACTTCTCC TTCTGTCTCT 960
TGGAAAGATA CAGCTCCAGG GTTAAAAAGA GAGTTTTTAG TGAAGTATCT TTCAGATAGC 1020
AGGCAGGGAA GCAATGTAGT GTGGTGGGCA GAGCCCCACA CAGAATCAGA AGGGATGAAT 1080
GGATGTCCCA GCCCAACCAC TAATTCACGT TATGGTCTTG ATCTATTTCT TCTGTTTTGA 1140
GAGCCTCCAG TTAATATGGG GCTTCAGTAC CAGAGCAGCT AGCAACTCTG CCCTAATGGG 1200
AAATGAAGGG GAGCTGGGTG TGAGTGTGTTA CACTGTGCCC TTCACGGGAT ACTTCTTTTA 1260
TCTGCAGATG GCCTAATGCT TAGTTGTCCA AGTCGCGATC AAGGACTCTC TCACACAGGA 1320
AACTTCCCTA TACTGGCAGA TACACTTGTG ACTGAACCAT GCCCAGTTTA TGCCTGTCTG 1380
ACTGTCACCT TGGCACTAGG AGGCTGATCT TGTACTCCAT ATGACCCAC CCCTAGGAAC 1440
CCCCAGGGAA AACCAGGCTC GGACAGCCCC CTGTTCCCTGA GATGGAAAGC ACAAATTTAA 1500
TACACCACCA CAATGGAAAA CAAGTTCAAA GACTTTTACT TACAGATCCT GGACAGAAAAG 1560
GGCATAATGA GTCTGAAGGG CAGTCCTCCT TCTCCAGGTT ACATGAGGCA GGAATAAGAA 1620
GTCAGACAGA GACAGCAAGA CAGTTAACAA CGTAGGTAAA GAAATAGGGT GTGGTCACTC 1680
TCAATTCACT GGCAAATGCC TGAATGGTCT GTCTGAAGGA AGCAACAGAG AAGTGGGGAA 1740
TCCAGTCTGC TAGGCAGGAA AGATGCCCTC AAGTTCTTGT CTCTGGCCAG AGGTGTGGTA 1800
TAGAACCAGA AACCATATC AAGGGTGACT AAGCCCGGCT TCCGGTATGA GAAATTAAAC 1860
TTGTATACAA AATGGTTGCC AAGGCAACAT AAAATTATAA GAATTC 1906

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1619 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GTCATGGAAT ACGCCTCTGA CGCTTCACTG GACCCCGAAG CCCCCTGGCC TCCCAGCCCC 60
CGCGCTCGCG CCGTCCCGCT ACTGCCCTTG GCCCTGGTCG CGGGGCTGCT GCTGCTGCTG 120
CTGCTCGCTG CCGCTGCGC CGTCTTCTC GCCTGCCCT GGGCCGTGTC CGGGGCTCGC 180
GCCTCGCCCG GCTCCGCGGC CAGCCCGAGA CTCCGCGAGG GTCCCGAGCT TTCGCCCCAG 240

GATCCCCGCCG	GCCTCTTGGA	CCTGCGGCAG	GGCATGTTTG	CGCAGCTGGT	GGCCCCAAAT	300
GTTCTGCTGA	TCGATGGGCC	CCTGAGCTGG	TACAGTGACC	CAGGCCTGGC	AGGCGTGTCC	360
CTGACGGGGG	GCCTGAGCTA	CAAAGAGGAC	ACGAAGGAGC	TGGTGGTGCC	CAAGGCTGGA	420
GTCTACTATG	TCTTCTTTCA	ACTAGAGCTG	CGGCGCGTGG	TGGCCGGCGA	GGGCTCAGGC	480
TCCGTTTCAC	TTGCGCTGCA	CCTGCAGCCA	CTGCGCTCTG	CTGCTGGGGC	CGCCGCCCTG	540
GCTTTGACCG	TGGACCTGCC	ACCCGCTCC	TCCGAGGCTC	GGAACCTCGC	CTTCGGTTTC	600
CAGGGCCGCT	TGCTGCACCT	GAGTGCCGGC	CAGCGCCTGG	GCGTCCATCT	TCACACTGAG	660
GCCAGGGCAC	GCCATGCCTG	GCAGCTTACC	CAGGGCGCCA	CAGTCTTGGG	ACTCTTCCGG	720
GTGACCCCCG	AAATCCCAGC	CGGACTCCCT	TCACCGAGGT	CGGAATAACG	CCCAGCCTGG	780
GTGCAGCCCA	CCTGGACAGA	GTCCGAATCC	TACTCCATCC	TTCATGGAGA	CCCCTGGTGC	840
TGGGTCCCCTG	CTGCTTTCTC	TACCTCAAGG	GGCTTGGCAG	GGGTCCCTGC	TGCTGACCTC	900
CCCTTGAGGA	CCCTCCTCAC	CCACTCCTTC	CCCAAGTTGG	ACCTTGATAT	TTATTCTGAG	960
CCTGAGCTCA	GATAATATAT	TATATATATT	ATATATATAT	ATATATTTCT	ATTTAAAGAG	1020
GATCCTGAGT	TTGTGAATGG	ACTTTTTTAG	AGGAGTTGTT	TTGGGGGGGG	GGTCTTCGAC	1080
ATTGCCGAGG	CTGGTCTTGA	ACTCCTGGAC	TTAGACGATC	CTCCTGCCTC	AGCCTCCCAA	1140
GCAACTGGGA	TTCATCCTTT	CTATTAAATC	ATTGTACTTA	TTTGCCATT	TGTGTGTATT	1200
GAGCATCTGT	AATGTGCCAG	CATTGTGCCC	AGGCTAGGGG	GCTATAGAAA	CATCTAGAAA	1260
TAGACTGAAA	GAAAATCTGA	GTTATGGTAA	TACGTGAGGA	ATTTAAAGAC	TCATCCCCAG	1320
CCTCCACCTC	CTGTGTGATA	CTTGGGGGCT	AGCTTTTTTC	TTTCTTTCTT	TTTTTTGAGA	1380
TGGTCTTGTT	CTGTCAACCA	GGCTAGAATG	CAGCGGTGCA	ATCATGAGTC	AATGCAGCCT	1440
CCAGCCTCGA	CCTCCCAGAG	CTCAGGTGAT	CCTCCCATCT	CAGCCTCTCG	AGTAGCTGGG	1500
ACCACAGTTG	TGTGCCACCA	CACCTGGCTA	ACTTTTTAAT	TTTTTTGCGG	AGACGGTATT	1560
GCTATGTTGC	CAAGGTTGTT	TACATGCCAG	TACAAATTAT	AATAAACACT	CATTTTTTCC	1619

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1239 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

AGCCTATAAA	GCACGGGCAC	TGGCGGGAGA	CGTGCACTGA	CCGACCGTGG	TAATGGACCA	60
GCACACACTT	GATGTGGAGG	ATACCGCGGA	TGCCAGACAT	CCAGCAGGTA	CTTCGTGCCC	120
CTCGGATGCG	GCGCTCCTCA	GAGATACCGG	GCTCCTCGCG	GACGCTGCGC	TCCTCTCAGA	180
TACTGTGCGC	CCCACAAATG	CCGCGCTCCC	CACGGATGCT	GCCTACCCTG	CGGTTAATGT	240
TCGGGATCGC	GAGGCCGCGT	GGCCGCTGTC	ACTGAACTTC	TGTTCCCGCC	ACCCAAAGCT	300
CTATGGCCTA	GTCGCTTTGG	TTTTGCTGCT	TCTGATCGCC	GCCTGTGTTC	CTATCTTCAC	360
CCGCACCGAG	CCTCGGCCAG	CGCTCACAAT	CACCACCTCG	CCCAACCTGG	GTACCCGAGA	420
GAATAATGCA	GACCAGGTCA	CCCCTGTTTC	CCACATTGGC	TGCCCCAACA	CTACACAACA	480
GGGCTCTCCT	GTGTTTCGCCA	AGCTACTGGC	TAAAAACCAA	GCATCGTTGT	GCAATACAAC	540
TCTGAACTGG	CACAGCCAAG	ATGGAGCTGG	GAGCTCATAC	CTATCTCAAG	GTCTGAGGTA	600
CGAAGAAGAC	AAAAAGGAGT	TGGTGGTAGA	CAGTCCCGGG	CTCTACTACG	TATTTTTTGA	660
ACTGAAGCTC	AGTCCAACAT	TCACAAACAC	AGGCCACAAG	GTGCAGGGCT	GGGTCTCTCT	720
TGTTTTGCAA	GCAAAGCCTC	AGGTAGATGA	CTTTGACAAC	TTGGCCCTGA	CAGTGGAACT	780
GTTCCCTTGC	TCCATGGAGA	ACAAGTTAGT	GGACCGTTCC	TGGAGTCAAC	TGTTGCTCCT	840
GAAGGCTGGC	CACCGCCTCA	GTGTGGGTCT	GAGGGCTTAT	CTGCATGGAG	CCCAGGATGC	900
ATACAGAGAC	TGGGAGCTGT	CTTATCCCAA	CACCACCAGC	TTTGGACTCT	TTCTTGTGAA	960
ACCCGACAAC	CCATGGGAAT	GAGAACTATC	CTTCTTGTA	CTCCTAGTTG	CTAAGTCCCT	1020
AAGCTGCTAT	GTTTTATGGG	GTCTGAGCAG	GGGTCCCTTC	CATGACTTTC	TCTTGTCTTT	1080
AACTGGACTT	GGTATTTATT	CTGAGCATAG	CTCAGACAAG	ACTTTATATA	ATTCAC TAGA	1140
TAGCATTAGT	AAACTGCTGG	GCAGCTGCTA	GATAAAAAAA	AATTTCTAAA	TCAAAGTTTA	1200
TATTTATATT	AATATATAAA	AATAAATGTG	TTTGTAAAT			1239

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 606 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ATGATCGAAA	CATACAACCA	AACTTCTCCC	CGATCTGCGG	CCACTGGACT	GCCCATCAGC	60
ATGAAAATTT	TTATGTATTT	ACTTACTGTT	TTTCTTATCA	CCCAGATGAT	TGGGTCAGCA	120
CTTTTGTCTG	TGTATCGCTT	CGCACAGGCT	TTTGAAATGC	AAAAAGGTGA	TCAGAATCCT	180
CAAATTGCGG	CACATGTCAT	AAGTGAGGCC	AGCAGTAAAA	CAACATCTGT	GTTACAGTGG	240
GCTGAAAAAG	GATACTACAC	CATGAGCAAC	AACTTGGTAA	CCCTGGAAAA	TGGGAAACAG	300
CTGACCGTTA	AAAGACAAGG	ACTCTATTAT	ATCTATGCCC	AAGTCACCTT	CTGTTCCAAT	360
CGGGAAGCTT	CGAGTCAAGC	TCCATTTATA	GCCAGCCTCT	GCCTAAAGTC	CCCCGGTAGA	420
TTGAGAGAG	TCTTACTCAG	AGCTGCAAAT	ACCCACAGTT	CCGCCAAACC	TTGCGGGCAA	480
CAATCCATTC	ACTTGGGAGG	AGTATTTGAA	TTGCAACCAG	GTGCTTCGGT	GTTTGTCAAT	540
GTGACTGATC	CAAGCCAAGT	GAGCCATGGC	ACTGGCTTCA	CGTCCTTTGG	CTTACTCAAA	600
CTCTGA						606

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 783 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

ATGATCGAAA	CATACAACCA	AACTTCTCCC	CGATCTGCGG	CCACTGGACT	GCCCATCAGC	60
ATGAAAATTT	TTATGTATTT	ACTTACTGTT	TTTCTTATCA	CCCAGATGAT	TGGGTCAGCA	120
CTTTTGTCTG	TGTATCTTCA	TAGAAGATTG	GATAAGGTCG	AAGAGGAAGT	AAACCTTCAT	180
GAAGATTTTG	TATTCATAAA	AAAGCTAAAG	AGATGCAACA	AAGGAGAAGG	ATCTTTATCC	240
TTGCTGAACT	GTGAGGAGAT	GAGAAGGCAA	TTTGAAGACC	TTGTCAAGGA	TATAACGTTA	300
AACAAAGAAG	AGAAAAAGA	AAACAGCTTT	GAAATGCAAA	AAGGTGATCA	GAATCCTCAA	360
ATTGCGGCAC	ATGTCATAAG	TGAGGCCAGC	AGTAAAACAA	CATCTGTGTT	ACAGTGGGCT	420
GAAAAAGGAT	ACTACACCAT	GAGCAACAAC	TTGGTAACCC	TGGAAAATGG	GAAACAGCTG	480
ACCGTTAAAA	GACAAGGACT	CTATTATATC	TATGCCCAAG	TCACCTTCTG	TTCCAATCGG	540
GAAGCTTCGA	GTCAAGCTCC	ATTTATAGCC	AGCCTCTGCC	TAAAGTCCCC	CGGTAGATTG	600
GAGAGAATCT	TACTCAGAGC	TGCAAATACC	CACAGTTCCG	CCAAACCTTG	CGGGCAACAA	660
TCCATTCACT	TGGGAGGAGT	ATTTGAATTG	CAACCAGGTG	CTTCGGTGTT	TGTCAATGTG	720
ACTGATCCAA	GCCAAGTGAG	CCATGGCACT	GGCTTCACGT	CCTTTGGCTT	ACTCAAACCT	780
TGA						783

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 558 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

CTGCTGCACT	TCGGGGTAAT	CGGCCCCCAG	AGGGAAGAGC	AGTCCCCAGG	TGGCCCCCTCC	60
ATCAACAGCC	CTCTGGTTCA	AACACTCAGG	TCCTCTTCTC	AAGCCTCAAG	TAACAAGCCG	120
GTAGCCACG	TTGTAGCCGA	CATCAACTCT	CCGGGGCAGC	TCCGGTGGTG	GGACTCGTAT	180
GCCAATGCCC	TCATGGCCAA	CGGTGTGAAG	CTGGAAGACA	ACCAGCTGGT	GGTGCCTGCT	240
GACGGGCTTT	ACCTCATCTA	CTCACAGGTC	CTCTTCAGGG	GCCAAGGCTG	CCCTTCCACC	300
CCCTTGTTCC	TCACCCACAC	CATCAGCCGC	ATTGCAGTCT	CCTACCAGAC	CAAGGTCAAC	360
ATCCTGTCTG	CCATCAAGAG	CCCTTGCCAC	AGGGAGACCC	CAGAGTGGGC	TGAGGCCAAG	420
CCCTGGTACG	AACCCATCTA	CCAGGGAGGA	GTCTTCCAGC	TGGAGAAGGG	AGATCGCCTC	480
AGTGCTGAGA	TCAACCTGCC	GGACTACCTG	GACTATGCCG	AGTCCGGGCA	GGTCTACTTT	540
GGGATCATTTG	CCCTGTGA					558

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	1783 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single
(D)	TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CAAGTCACAT	GATCCAGGAT	GCAGGGGAAA	ATCCTTCTTG	GAACAGAGCT	GGGTACAGAA	60
CCGAATCAGA	TGAGGAGAGA	TAAGGTGTGA	TGTGGGACAG	ACTATATAAA	GCATGGAGCC	120
AGGGCTGCAA	CAAGCAGGCA	GCTGTGGGGC	TCCTTCCCCT	GACCCAGCCA	TGCAGGTGCA	180
GCCCCGCTCG	GTAGCCAGCC	CCTGGAGAAG	CACGAGGCC	TGGAGAAGCA	CAAGTCGCAG	240
CTACTTCTAC	CTCAGCACCA	CCGCACGGT	GTGCCCTTGT	GTGGCAGTGG	CGATCATTTCT	300
GGTACTGGTA	GTCCAGAAAA	AGGACTCCAC	TCCAAATACA	ACTGAGAAGG	CCCCCTTAA	360
AGGAGGAAAT	TGCTCAGAGG	ATCTCTTCTG	TACCTTGAAA	AGTACTCCAT	CCAAGAAAGTC	420
ATGGGCCTAC	CTCCAAGTGT	CAAAGCATCT	CAACAATACC	AAACTGTCAT	GGAACGAAGA	480
TGGCACCATC	CACGGACTCA	TATACCAGGA	CGGGAACCTG	ATAGTCCAAT	TCCCTGGCTT	540
GTACTTTCATC	GTTTGCCAAC	TGCAGTTCCT	CGTGCAGTGC	TCAAATCATT	CTGTGGACCT	600
GACATTGCAG	CTCCTCATCA	ATTCCAAGAT	CAAAAAGCAG	ACGTTGGTAA	CAGTGTGTGA	660
GTCTGGAGTT	CAGAGTAAGA	ACATCTACCA	GAATCTCTCT	CAGTTTTTGC	TGCATTACTT	720
ACAGGTCAAC	TCTACCATAT	CAGTCAGGGT	GGATAATTTT	CAGTATGTGG	ATACAAACAC	780
TTTCCCTCTT	GATAATGTGC	TATCCGTCTT	CTTATATAGT	AGCTCAGACT	GAATAGTTGT	840
TCTTAACCTT	TATGAAAATG	CTGTCTACCA	TACAGTACTT	CATCTGTCCA	AACATGGGCC	900
AAAGAAAATA	TTAGGACAAC	TCAAACTAAG	CATGTGAGTT	AGTGCACCTC	TCTTTCTGTC	960
CTTTTGGAATA	ATACAAACCC	AGGATTTAGA	AAGTGGAGTC	TCCTTCAGAT	GCACAAACAG	1020
GAAAGAATGT	GATATGTGCA	CAGAGACCTA	CTTGGGCACT	AGAAGGGGTG	TGAGTTGTCC	1080
CAGTATAACC	ACTAATTCAC	TGACCTTGAG	CCATTTTTTCC	TTCCCCCTGG	AACTTGGGGT	1140
CTGAATCTGG	AAAAGTAGGA	GATGAGATTT	ACATTTCCCC	AATATTTTCT	TCAACTCAGA	1200
AGACGAGACT	GTGGAGCTGA	GCTCCCTACA	CAGATGAAGG	CCTCCCATGG	CATGAGGAAA	1260
ATGATGGTAC	CAGTAATGTC	TGCTTGACTG	TCATCTCAGC	AAGTCCTAAG	GACTTCCATG	1320
CTGCCCTTGT	GAAAGATACT	CTAACCTCTT	GTAATGGGCA	AAGTGATCCT	GTCTCTCACT	1380
GAGGGGAGTA	GCTGCTGCCA	TCTCCTGAGA	CATACATGGA	GACATTTTCT	GCCCAAATTC	1440
CATTCTGTGT	GCAGTTTTTTA	AGTATTCCCC	CAAAAGTTCT	TGACAATGAG	AACTTTGAAT	1500
GTGGGAAGAG	CTTCTGGACA	GCAAACATTA	ACAGCTTCTC	CTGACCAGAG	AGACCATGCA	1560
AGCTTGGTCT	TAGACCCATC	AAGCTTGAGG	TTTCTACATT	GTGGGAGACA	GACTTTTGAC	1620
AAACCATTTG	AGTTGATGTC	TGGGCCCCTG	GGAGTTCCTC	TTCAAGTAAGG	AGAGCAAGCC	1680
GTTCTAGTGC	TGTGTCAGAG	GATGGAGTAA	AATAGACACT	TTTCTGAAGG	AAAGGAGAAC	1740
AAAGTTCCAG	AAAAAGGCTA	GAAAATGTTT	AAAAAGAAAA	AAA		1783

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1047 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

AGAGAGCGCT GGGAGCCGGA GGGGAGCGCA GCGAGTTTTG GCCAGTGGTC GTGCAGTCCA 60
AGGGGCTGGA TGGCATGCTG GACCCAAGCT CAGCTCAGCG TCCGGACCCA ATAACAGTTT 120
TACCAAGGGA GCAGCTTCT ATCCTGGCCA CACTGAGGTG CATAGCGTAA TGTCCATGTT 180
GTTCTACAG CTGATCACAG CTTTCTGAT CGGCATACAG GCGGAACCAC ACTCAGAGAG 240
CAATGTCCCT GCAGGACACA CCATCCCCCA AGTCCACTGG ACTAAACTTC AGCATTCCCT 300
TGACACTGCC CTTGCGCAGAG CCCGCGAGCG CCCGGCAGCG GCGATAGCTG CACGCGTGGC 360
GGGGCAGACC CGCAACATTA CTGTGGACCC CAGGCTGTTT AAAAAGCGGC GACTCCGTTC 420
ACCCCGTGTG CTGTTTAGCA CCCAGCCTCC CCGTGAAGCT GCAGACACTC AGGATCTGGA 480
CTTCGAGGTC GGTGGTGCTG CCCCTTCAA CAGGACTCAC AGGAGCAAGC GGTCAATCATC 540
CCATCCCATC TTCCACAGGG GCGAATTCTC GGTGTGTGAC AGTGTGAGCG TGTGGGTGG 600
GGATAAGACC ACCGCCACAG ACATCAAGGG CAAGGAGGTG ATGGTGTGG GAGAGGTGAA 660
CATTAAACAAC AGTGTATTCA AACAGTACTT TTTTGAGACC AAGTGCCGGG ACCCAAATCC 720
CGTTGACAGC GGGTGCCGGG GCATTGACTC AAAGCACTGG AACTCATATT GTACCACGAC 780
TCACACCTTT GTCAGGCGC TGACCATGGA TGGCAAGCAG GCTGCCCTGGC GGTTTATCCG 840
GATAGATACG GCCTGTGTGT GTGTGCTCAG CAGGAAGGCT GTGAGAAGAG CCTGACCTGC 900
CGACACGCTC CCTCCCCCTG CCCCTTCTAC ACTCTCCTGG GCCCCCTCCCT ACCTCAACCT 960
GTAAATTATT TTAAATTATA AGGACTGCAT GGTAATTTAT AGTTTATACA GTTTTAAAGA 1020
ATCATTATTT ATTAAATTTT TGGAAGC 1047

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1176 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

GAGCGCCTGG AGCCGGAGGG GAGCGCATCG AGTGACTTTG GAGCTGGCCT TATATTTGGA 60
TCTCCCGGGC AGCTTTTTTG AAACCTCCTAG TGAACATGCT GTGCCTCAAG CCAGTGAAAT 120
TAGGCTCCCT GGAGGTGGGA CACGGGCAGC ATGGTGGAGT TTTGGCCTGT GGTGCTGCAG 180
TCCAGGGGGC TGGATGGCAT GCTGGACCCA AGCTCACCTC AGTGTCTGGG CCCAATAAAG 240
GTTTTTGCCAA GGACGCAGCT TTCTATACTG GCCGCACTGA GGTGCATAGC GTAATGTCCA 300
TGTTGTTCTA CACTCTGATC ACTGCGTTTT TGATCGGCGT ACAGGCAGAA CCGTACACAG 360
ATAGCAATGT CCCAGAAGGA GACTCTGTCC CTGAAGCCCA CTGGACTAAA CTTTACGATT 420
CCCTTGACAC AGCCCTCCGC AGAGCCCGCA GTGCCCCTAC TGCACCAATA GCTGCCCCGAG 480
TGACAGGGCA GACCCGCAAC ATCACTGTAG ACCCCAGACT GTTTAAGAAA CGGAGACTCC 540
ACTCACCCCG TGTGCTGTTT AGCACCAGC CTCCACCCAC CTCTTCAGAC ACTCTGGATC 600
TAGACTTCCA GGCCCATGGT ACAATCCCTT TCAACAGGAC TCACCGGAGC AAGCGCTCAT 660
CCACCCACCC AGTCTTCCAC ATGGGGGAGT TCTCAGTGTG TGACAGTGTG AGTGTGTGGG 720
TTGGAGATAA GACCACAGCC ACAGACATCA AGGGCAAGGA GGTGACAGTG CTGGCCGAGG 780
TGAACATTAA CAACAGTGTA TTCAGACAGT ACTTTTTTTGA GACCAAGTGC CGAGCCTCCA 840
ATCCTGTTGA GAGTGGGTGC CGGGGCATCG ACTCCAAACA CTGGAACCTCA TACTGCACCA 900
CGACTCACAC CTTGCTCAAG GCGTTGACAA CAGATGAGAA GCAGGCTGCC TGGAGGTTCA 960
TCCGGATAGA CACAGCCTGT GTGTGTGTGC TCAGCAGGAA GGCTACAAGA AGAGGCTGAC 1020

TTGCCTGCAG	CCCCCTTCCC	CACCTGCCCC	CTCCACACTC	TCTTGGGCCC	CTCCCTACCT	1080
CAGCCTGTAA	ATTATTTTAA	ATTATAAGGA	CTGCATGATA	ATTTATCGTT	TATACAATTT	1140
TAAAGACATT	ATTTATTAAA	TTTTCAAAGC	ATCCTG			1176

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	1623 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single
(D)	TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

TCAGAGTCCT	GTCCTTGACA	CTTCAGTCTC	CACAAGACTG	AGAGGAGGAA	ACCCTTTCCT	60
GGGGCTGGGT	GCCATGCAGC	AGCCCGTGAA	TTACCCATGT	CCCCAGATCT	ACTGGGTAGA	120
CAGCAGTGCC	ACTTCTCCTT	GGGCTCCTCC	AGGGTCAGTT	TTTTCTTGTC	CATCCTCTGG	180
GCCTAGAGGG	CCAGGACAAA	GGAGACCACC	GCCTCCACCA	CCACCTCCAT	CACCACTACC	240
ACCGCCTTCC	CAACCACCCC	CGCTGCCTCC	ACTAAGCCCT	CTAAAGAAGA	AGGACAACAT	300
AGAGCTGTGG	CTACCGGTGA	TATTTTTCAT	GGTGCTGGTG	GCTCTGGTTG	GAATGGGGTT	360
AGGAATGTAT	CAACTCTTTC	ATCTACAGAA	GGAAGTGGCA	GAAGTCCGTG	AGTTCACCAA	420
CCACAGCCTT	AGAGTATCAT	CTTTTGAAAA	GCAAATAGCC	AACCCAGCA	CACCCCTCTGA	480
AACCAAAAAG	CCAAGGAGTG	TGGCCCACTT	AACAGGGAAC	CCCCGCTCAA	GGTCCATCCC	540
TCTGGAATGG	GAAGACACAT	ATGGAACTGC	TTTGATCTCT	GGAGTGAAGT	ATAAGAAAAG	600
CGGCCTTGTG	ATCAATGAGG	CTGGGTGTGA	CTTCGTATAT	TCCAAAGTAT	ACTTCCGGGG	660
TCAGTCTTGC	AACAGCCAGC	CCCTAAGCCA	CAAGGTCTAT	ATGAGGAACT	TTAAGTATCC	720
TGGGGATCTG	GTGCTAATGG	AGGAGAAGAA	GTTGAATTAC	TGCACTACTG	GCCAGATATG	780
GGCCACAGC	AGCTACCTAG	GGGCAGTATT	TAATCTTACC	GTTGCTGACC	ATTTATATGT	840
CAACATATCT	CAACTCTCTC	TGATCAATTT	TGAGGAATCT	AAGACCTTTT	TTGGCTTATA	900
TAAGCTTTAA	AGGAAAAAGC	ATTTTAGAAT	GATCTATTAT	TCTTTATCAT	GGATGCCAGG	960
AATATTGTCT	TCAATGAGAG	TCTTCTTAAG	ACCAATTGAG	CCACAAAGAC	CACAAGGTCC	1020
AACAGGTCAG	CTACCCTTCA	TTTTCTAGAG	GTCCATGGAG	TGGTCCTTAA	TGCCGTGCATC	1080
ATGAGCCAGA	TGGGAAGAAG	ACTGTTCCCTG	AGGAACATAA	AGTTTTGGGC	TGCTGTGTGG	1140
CAATGCAGAG	GCAAAGAGAA	GGAAGTGTCT	GATGTTAAAT	GGCCAAGAGC	ATTTTAGCCA	1200
TTGAAGAAAA	AAAAAACCTT	TAAACTCACC	TTCCAGGGTG	GGTCTACTTG	CTACCTCACA	1260
GGAGGCCGTC	TTTTTAGACAC	ATGGTTGTGG	TATGACTATA	CAAGGGTGAG	AAAGGATGCT	1320
AGGTTTTCATG	GATAAGCTAG	AGACTGAAAA	AAGCCAGTGT	CCCATTTGGCA	TCATCTTTAT	1380
TTTTAACTGA	TGTTTTCTGA	GCCCACCTTT	GATGCTAACA	GAGAAATAAG	AGGGGTGTTT	1440
GAGGCACAAG	TCATTCTCTA	CATAGCATGT	GTACCTCCAG	TGCAATGATG	TCTGTGTGTG	1500
TTTTTATGTA	TGAGAGTAGA	GCGATTCTAA	AGAGTCACAT	GAGTACAACG	CGTACATTAC	1560
GGAGTACATA	TTAGAAAAGT	ATGTGTTACA	TTTGATGCTA	GAATATCTGA	ATGTTTCTTG	1620
CTA						1623

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	28 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single
(D)	TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

GTTAAGCTTT TCAGTCAGCA TGATAGAA

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

GTTTCTAGAT CAGAGTTTGA GTAAGCC

27

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

CCAAGACTAG TTAACACAGC ATGATCGAAA

30

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

CCAATGCGGC CGCACTCAGA ATTCAACCTG

30

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 972 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

TCTAGACTCA GGACTGAGAA GAAGTAAAAC CGTTTGCTGG GGCTGGCCTG ACTCACCAGC 60
TGCCATGCAG CAGCCCTTCA ATTACCCATA TCCCAGATC TACTGGGTGG ACAGCAGTGC 120
CAGCTCTCCC TGGGCCCTC CAGGCACAGT TCTTCCCTGT CCAACCTCTG TGCCCAGAAG 180

GCCTGGTCAA	AGGAGGCCAC	CACCACCACC	GCCACCGCCA	CCACTACCAC	CTCCGCCGCC	240
GCCGCCACCA	CTGCCTCCAC	TACCGCTGCC	ACCCCTGAAG	AAGAGAGGGA	ACCACAGCAC	300
AGGCCTGTGT	CTCCTTGTGA	TGTTTTTCAT	GGTCTGGTT	GCCTTGGTAG	GATTGGGCCT	360
GGGGATGTTT	CAGCTCTTCC	ACCTACAGAA	GGAGCTGGCA	GAATCCGAG	AGTCTACCAG	420
CCAGATGCAC	ACAGCATCAT	CTTTGGAGAA	GCAAATAGGC	CACCCCAGTC	CACCCCCTGA	480
AAAAAAGGAG	CTGAGGAAAAG	TGGCCCATTT	AACAGGCAAG	TCCAAC TCAA	GGTCCATGCC	540
TCTGGAATGG	GAAGACACCT	ATGGAATTGT	CCTGCTTTCT	GGAGTGAAGT	ATAAGAAGGG	600
TGGCCTTGTG	ATCAATGAAA	CTGGGCTGTA	CTTTGTATAT	TCCAAAGTAT	ACTTCCGGGG	660
TCAATCTTGC	AACAACCTGC	CCCTGAGCCA	CAAGGTCTAC	ATGAGGAACT	CTAAGTATCC	720
CCAGGATCTG	GTGATGATGG	AGGGGAAGAT	GATGAGCTAC	TGCACTACTG	GGCAGATGTG	780
GGCCCCGAGC	AGCTACCTGG	GGGCAGTGTT	CAATCTTACC	AGTGCTGATC	ATTTATATGT	840
CAACGTATCT	GAGCTCTCTC	TGGTCAATTT	TGAGGAATCT	CAGACGTTTT	TCGGCTTATA	900
TAAGCTCTAA	GAGAAGCACT	TTGGGATTCT	TTCCATTATG	ATTCTTTGTT	ACAGGCACCG	960
AGATGTTCTA	GA					972

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	885 base pairs
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

ATGCAGCAGC	CCATGAATTA	CCCATGTCCC	CAGATCTTCT	GGGTAGACAG	CAGTGCCACT	60
TCATCTTGGG	CTCCTCCAGG	GTCAGTTTTT	CCCTGTCCAT	CTTGTGGGCC	TAGAGGGCCG	120
GACCAAAGGA	GACCGCCACC	TCCACCACCA	CCTGTGTAC	CACTACCACC	GCCATCACAA	180
CCACTCCCAC	TGCCGCCACT	GACCCCTCTA	AAGAAGAAGG	ACCACAACAC	AAATCTGTGG	240
CTACCGGTGG	TATTTTTCAT	GGTCTGGTG	GCTCTGGTTG	GAATGGGATT	AGGAATGTAT	300
CAGCTCTTCC	ACCTGCAGAA	GGAAC TGGCA	GAACTCCGTG	AGTTCACCAA	CCAAAGCCTT	360
AAAGTATCAT	CTTTTGAAAA	GCAAATAGCC	AACCCCAGTA	CACCCCTCTGA	AAAAAAGAG	420
CCGAGGAGTG	TGGCCCATTT	AACAGGGAAC	CCCCACTCAA	GGTCCATCCC	TCTGGAATGG	480
GAAGACACAT	ATGGAACCGC	TCTGATCTCT	GGAGTGAAGT	ATAAGAAAGG	TGGCCTTGTG	540
ATCAACGAAG	CTGGGTTGTA	CTTCGTATAT	TCCAAAGTAT	ACTTCCGGGG	TCAGTCTTGC	600
AACAACCAGC	CCCTAAACCA	CAAGGTCTAT	ATGAGGAACT	CTAAGTATCC	TGGGGATCTG	660
GTGCTAATGG	AGGAGAAGAG	GTTGAACTAC	TGCACTACTG	GACAGATATG	GGCCCACAGC	720
AGCTACCTGG	GGGCAGTATT	CAATCTTACC	AGTGCTGACC	ATTTATATGT	CAACATATCT	780
CAACTCTCTC	TGATCAATTT	TGAGGAATCT	AAGACCTTTT	TCGGCTTGTA	TAAGCTTTAA	840
AAGAAAAAGC	ATTTTAAAAAT	GATCTACTAT	TCTTTATCAT	GGGCA		885

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	29 base pairs
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

CTTAAGCTTC TACAGGACTG AGAAGAAGT

29

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	30 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single
(D)	TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CTTGAATTCC AACATTCTCG GTGCCTGTAA

30

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	27 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single
(D)	TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

TCAGGATCCA CAAGGCTGTG AGAAGGA

27

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	26 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single
(D)	TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

CTTGTCTAGA CCTGGTGCCC ATGATA

26

2022-02-28 14:28:30

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 680 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

ATGCCGGAGG	AAGGTCGCCC	TTGCCCCCTGG	GTTTCGCTGGA	GCGGGACCGC	GTTCCAGCGC	60
CAATGGCCAT	GGCTGCTGCT	GGTGGTGTTT	ATTACTGTGT	TTTGCTGTTG	GTTTCATTGT	120
AGCGGACTAC	TCAGTAAGCA	GCAACAGAGG	CTGCTGGAGC	ACCCTGAGCC	GCACACAGCT	180
GAGTTACAGC	TGAATCTCAC	AGTTCCTCGG	AAGGACCCCA	CACTGCGCTG	GGGAGCAGGC	240
CCAGCCTTGG	GAAGGTCCTT	CACACACGGA	CCAGAGCTGG	AGGAGGGCCA	TCTGCGTATC	300
CATCAAGATG	GCCCTCTACG	GCTGCATATC	CAGGTGACAC	TGGCCAACTG	CTCTTCCCCA	360
GGCAGCACCC	TGCAGCACAG	GGCCACCCTG	GCTGTGGGCA	TCTGCTCCCC	CGCTGCGCAC	420
GGCATCAGCT	TGCTGCGTGG	GCGCTTTTGA	CAGGACTGTA	CAGTGGCATT	ACAGCGCCTG	480
ACATACCTGG	TCCACGGAGA	TGTCCTCTGT	ACCAACCTCA	CCCTGCCTCT	GCTGCCGTCC	540
CGCAACGCTG	ATGAGACCTT	CTTTGGAGTT	CAGTGGATAT	GCCCTTGACC	ACAACTCCAG	600
GATGACTTGT	GAATATTTTT	TTTCTTTTCA	AGTTCACGT	ATTTATAAAT	GTATATAGTA	660
CACATAAAAA	AAAAAAAAAA					680

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 846 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

ATGCAGCAGC	CCTTCAATTA	CCCATATCCC	CAGATCTACT	GGGTGGACAG	CAGTGCCAGC	60
TCTCCCTGGG	CCCCCTCCAGG	CACAGTTCTT	CCCTGTCCAA	CCTCTGTGCC	CAGAAGGCCCT	120
GGTCAAAGGA	GGCCACCACC	ACCACCGCCA	CCGCCACCAC	TACCACCTCC	GCCGCCGCCG	180
CCACCACTGC	CTCCACTACC	GCTGCCACCC	CTGAAGAAGA	GAGGGAACCA	CAGCACAGGC	240
CTGTGTCTCC	TTGTGATGTT	TTTCATGGTT	CTGGTTGCCCT	TGGTAGGATT	GGGCCCTGGGG	300
ATGTTTCAGC	TCTTCCACCT	GCAGAAGGAA	CTGGCAGAAC	TCCGTGAGTT	CACCAACCAA	360
AGCCTTAAAG	TATCATCTTT	TGAAAAGCAA	ATAGGCCACC	CCAGTCCACC	CCCTGAAAAA	420
AAGGAGCTGA	GGAAGTGCC	CCATTTAACA	GGCAAGTCCA	ACTCAAGGTC	CATGCCCTCTG	480
GAATGGGAAG	ACACCTATGG	AATTGTCTCTG	CTTTCTGGAG	TGAAGTATAA	GAAGGGTGGC	540
CTTGTGATCA	ATGAACTGG	GCTGTACTTT	GTATATTCCA	AAGTATACTT	CCGGGGTCAA	600
TCTTGCAACA	ACCTGCCCCCT	GAGCCACAAG	GTCTACATGA	GGAACTCTAA	GTATCCCCAG	660
GATCTGGTGA	TGATGGAGGG	GAAGATGATG	AGCTACTGCA	CTACTGGGCA	GATGTGGGCC	720
CGCAGCAGCT	ACCTGGGGGC	AGTGTTC AAT	CTTACCAGTG	CTGATCATTT	ATATGTCAAC	780
GTATCTGAGC	TCTCTCTGGT	CAATTTTGAG	GAATCTCAGA	CGTTTTTTCGG	CTTATATAAG	840
CTCTAA						846

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 786 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

ATGCAGCAGC	CCTTCAATTA	CCCATATCCC	CAGATCTACT	GGGTGGACAG	CAGTGCCAGC	60
TCTCCCTGGG	CCCCCTCCAGG	CACAGTTCTT	CCCTGTCCAA	CCTCTGTGCC	CAGAAGGCCT	120
GGTCAAAGGA	GGCCACCACC	ACCACCGCCA	CCGCCACCAC	TACCACCTCC	GCCGCCGCCG	180
CCACCACTGC	CTCCACTACC	GCTGCCACCC	CTGAAGAAGA	GAGGGAACCA	CAGCACAGGC	240
CTGTGTCTCC	TTGTGATGTT	TTTCATGGTT	CTGGTTGCCCT	TGGTAGGATT	GGGCCTGGGG	300
ATGTTTCAGC	TCTTCCGCTT	CGCACAGGCT	ATAGGCCACC	CCAGTCCACC	CCCTGAAAAA	360
AAGGAGCTGA	GGAAAGTGGC	CCATTTAACA	GGCAAGTCCA	ACTCAAGGTC	CATGCCTCTG	420
GAATGGGAAG	ACACCTATGG	AATTGTCTTG	CTTTCTGGAG	TGAAGTATAA	GAAGGGTGGC	480
CTTGTGATCA	ATGAAACTGG	GCTGTACTTT	GTATATTCCA	AAGTATACTT	CCGGGGTCAA	540
TCTTGCAACA	ACCTGCCCCT	GAGCCACAAG	GTCTACATGA	GGAACCTCTA	GTATCCCCAG	600
GATCTGGTGA	TGATGGAGGG	GAAGATGATG	AGCTACTGCA	CTACTGGGCA	GATGTGGGCC	660
CGCAGCAGCT	ACCTGGGGGC	AGTGTTC AAT	CTTACCAGTG	CTGATCATTT	ATATGTCAAC	720
GTATCTGAGC	TCTCTCTGGT	CAATTTTGAG	GAATCTCAGA	CGTTTTTCGG	CTTATATAAG	780
CTCTAA						786

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 864 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

ATGCAGCAGC	CCTTCAATTA	CCCATATCCC	CAGATCTACT	GGGTGGACAG	CAGTGCCAGC	60
TCTCCCTGGG	CCCCCTCCAGG	CACAGTTCTT	CCCTGTCCAA	CCTCTGTGCC	CAGAAGGCCT	120
GGTCAAAGGA	GGCCACCACC	ACCACCGCCA	CCGCCACCAC	TACCACCTCC	GCCGCCGCCG	180
CCACCACTGC	CTCCACTACC	GCTGCCACCC	CTGAAGAAGA	GAGGGAACCA	CAGCACAGGC	240
CTGTGTCTCC	TTGTGATGTT	TTTCATGGTT	CTGGTTGCCCT	TGGTAGGATT	GGGCCTGGGG	300
ATGTTTCAGC	TCTTCCAATC	CTCCATCCTC	CCCTATGCCG	GAGGAGGGTT	CGGGCTGCTC	360
GGTGCGGCGC	AGGCCCTATG	GGTGCGTCCT	GCGGCCATCC	TCAATCCTAT	AGGCCACCCC	420
AGTCCACCCC	CTGAAAAAAA	GGAGCTGAGG	AAAGTGGCCC	ATTTAACAGG	CAAGTCCAAC	480
TCAAGGTCCA	TGCCTCTGGA	ATGGGAAGAC	ACCTATGGAA	TTGTCCTGCT	TTCTGGAGTG	540
AAGTATAAGA	AGGGTGGCCT	TGTGATCAAT	GAAACTGGGC	TGTACTTTGT	ATATTCCAAA	600
GTATACTTCC	GGGGTCAATC	TTGCAACAAC	CTGCCCCTGA	GCCACAAGGT	CTACATGAGG	660
AACTCTAAGT	ATCCCCAGGA	TCTGGTGATG	ATGGAGGGGA	AGATGATGAG	CTACTGCACT	720
ACTGGGCAGA	TGTGGGCCCG	CAGCAGCTAC	CTGGGGGCAG	TGTTCAATCT	TACCAGTGCT	780
GATCATTTAT	ATGTCAACGT	ATCTGAGCTC	TCTCTGGTCA	ATTTTGAGGA	ATCTCAGACG	840
TTTTTCGGCT	TATATAAGCT	CTAA				864

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 828 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

ATGCAGCAGC	CCTTCAATTA	CCCATATCCC	CAGATCTACT	GGGTGGACAG	CAGTGCCAGC	60
TCTCCCTGGG	CCCCTCCAGG	CACAGTTCTT	CCCTGTCCAA	CCTCTGTGCC	CAGAAGGCCT	120
GGTCAAAGGA	GGCCACCACC	ACCACCGCCA	CCGCCACCAC	TACCACCTCC	GCCGCCGCCG	180
CCACCCTGTC	CTCCACTACC	GCTGCCACCC	CTGAAGAAGA	GAGGGAACCA	CAGCACAGGC	240
CTGTGTCTCC	TTGTGATGTT	TTTCATGGTT	CTGGTTGCCT	TGGTAGGATT	GGGCCTGGGG	300
ATGTTTCAGC	TCTTCCACCT	ACAGCGAGAG	TCTACCAGCC	AGATGCACAC	AGCATCATCT	360
TTGGAGAAGC	AAATAGGCCA	CCCCAGTCCA	CCCCCTGAAA	AAAAGGAGCT	GAGGAAAGTG	420
GCCCATTTAA	CAGGCAAGTC	CAACTCAAGG	TCCATGCCTC	TGGAATGGGA	AGACACCTAT	480
GGAATTGTCC	TGCTTTCTGG	AGTGAAGTAT	AAGAAGGGTG	GCCTTGTGAT	CAATGAAACT	540
GGGCTGTACT	TTGTATATTC	CAAAGTATAC	TTCCGGGGTC	AATCTTGCAA	CAACCTGCCC	600
CTGAGCCACA	AGGTCTACAT	GAGGAACTCT	AAGTATCCCC	AGGATCTGGT	GATGATGGAG	660
GGGAAGATGA	TGAGCTACTG	CACTACTGGG	CAGATGTGGG	CCCGCAGCAG	CTACCTGGGG	720
GCAGTGTTC	ATCTTACCAG	TGCTGATCAT	TTATATGTCA	ACGTATCTGA	GCTCTCTCTG	780
GTCAATTTTG	AGGAATCTCA	GACGTTTTTC	GGCTTATATA	AGCTCTAA		828

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 846 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

ATGGCTATGA	TGGAGGTCCA	GGGGGGACCC	AGCCTGGGAC	AGACCTGCGT	GCTGATCGTG	60
ATCTTCACAG	TGCTCCTGCA	GTCTCTCTGT	GTGGCTGTAA	CTTACGTGTA	CTTTACCAAC	120
GAGCTGAAGC	AGATGCAGGA	CAAGTACTCC	AAAAGTGGCA	TTGCTTGTTT	CTTAAAAGAA	180
GATGACAGTT	ATTGGGACCC	CAATGACGAA	GAGAGTATGA	ACAGCCCCTG	CTGGCAAGTC	240
AAGTGGCAAC	TCCGTCAGCT	CGTTAGAAAG	ATGATTTTGA	GAACCTCTGA	GGAAACCATT	300
TCTACAGTTC	AAGAAAAGCA	ACAAAATATT	TCTCCCCTAG	TGAGAGAAAG	AGGTCCCTCAG	360
AGAGTAGCAG	CTCACATAAC	TGGGACCAGA	GGAAGAAGCA	ACACATTGTC	TTCTCCAAAC	420
TCCAAGAATG	AAAAGGCTCT	GGGCCGCAAA	ATAAAC'TCCT	GGGAATCATC	AAGGAGTGGG	480
CATTCA'TTCC	TGAGCAACTT	GCACTTGAGG	AATGGTGAAC	TGGTCATCCA	TGAAAAAGGG	540
TTTTACTACA	TCTATTCCCA	AACATACTTT	CGATTTTCAGG	AGGAAATAAA	AGAAAACACA	600
AAGAACGACA	AACAAATGGT	CCAATATATT	TACAAATACA	CAAGTTATCC	TGACCC'TATA	660
TTGTTGATGA	AAAGTGCTAG	AAATAGTTGT	TGGTCTAAAG	ATGCAGAATA	TGGACTCTAT	720
TCCATCTATC	AAGGGGGAAT	ATTTGAGCTT	AAGGAAAATG	ACAGAATTTT	TGTTTCTGTA	780
ACAAATGAGC	ACTTGATAGA	CATGGACCAT	GAAGCCAGTT	TTTTTCGGGGC	CTTTT'TAGTT	840
GGCTAA						846

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 876 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

ATGCCTTCCT	CAGGGGCCCT	GAAGGACCTC	AGCTTCAGTC	AGCACTTCAG	GATGATGGTG	60
ATTTGCATAG	TGCTCCTGCA	GGTGCTCCTG	CAGGCTGTGT	CTGTGGCTGT	GACTTACATG	120
TACTTCACCA	ACGAGATGAA	GCAGCTGCAG	GACAATTACT	CCAAAATTGG	ACTAGCTTGC	180
TTCTCAAAGA	CGGATGAGGA	TTTCTGGGAC	TCCACTGATG	GAGAGATCTT	GAACAGACCC	240
TGCTTGCAAG	TTAAGAGGCA	ACTGTATCAG	CTCAATTGAAG	AGGTGACTTT	GAGAACCCTT	300
CAGGACACCA	TTTCTACAGT	TCCAGAAAAG	CAGCTAAGTA	CTCCTCCCTT	GCCCAGAGGT	360
GGAAGACCTC	AGAAAGTGGC	AGCTCACATT	ACTGGGATCA	CTCGGAGAAG	CAACTCAGCT	420
TTAATTCCAA	TCTCCAAGGA	TGGAAGACC	TTAGGCCAGA	AGATTGAATC	CTGGGAGTCC	480
TCTCGGAAAG	GGCATTTCATT	TCTCAACCAC	GTGCTCTTTA	GGAATGGAGA	GCTGGTCATC	540
GAGCAGGAGG	GCCTGTATTA	CATCTATTCC	CAAACATACT	TCCGATTTCA	GGAAGCTGAA	600
GACGCTTCCA	AGATGGTCTC	AAAGGACAAG	GTGAGAACCA	AACAGCTGGT	GCAGTACATC	660
TACAAGTACA	CCAGCTATCC	GGATCCCATA	GTGCTCATGA	AGAGCGCCAG	AAACAGCTGT	720
TGGTCCAGAG	ATGCCGAGTA	CGGACTGTAC	TCCATCTATC	AGGGAGGATT	GTTCCGAGCTA	780
AAAAAAAAATG	ACAGGATTTT	TGTTTCTGTG	ACAAATGAAC	ATTTGATGGA	CCTGGATCAA	840
GAAGCCAGCT	TCTTTGGAGC	CTTTTAAATT	AACTAA			876

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 720 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

ATGGAGCCAG	GGCTGCAACA	AGCAGGCAGC	TGTGGGGCTC	CTTCCCCTGA	CCCAGCCATG	60
CAGGTGCAGC	CCGGCTCGGT	AGCCAGCCCC	TGGAGAAGCA	CGAGGCCCTG	GAGAAGCACA	120
AGTCGCAGCT	ACTTCTACCT	CAGCACCACC	GCCTTGGTGT	GCCTTGTGTG	GGCAGTGGCG	180
ATCATTCTGG	TACTGGTAGT	CCAGAAAAAG	GACTCCACTC	CAAATACAAC	TGAGAAGGCC	240
CCCCTTAAAG	GAGGAAATTG	CTCAGAGGAT	CTCTTCTGTA	CCCTGAAAAG	TACTCCATCC	300
AAGAAGTCAT	GGGCCTACCT	CCAAGTGTCA	AAGCATCTCA	ACAATACCAA	ACTGTCATGG	360
AACGAAGATG	GCACCATCCA	CGGACTCATA	TACCAGGACG	GGAACCTGAT	AGTCCAATTC	420
CCTGGCTTGT	ACTTCATCGT	TTGCCAACTG	CAGTTCCTCG	TGCAGTGCTC	AAATCATTCT	480
GTGGACCTGA	CATTGCAGCT	CCTCATCAAT	TCCAAGATCA	AAAAGCAGAC	GTTGGTAACA	540
GTGTGTGAGT	CTGGAGTTCA	GAGTAAGAAC	ATCTACCAGA	ATCTCTCTCA	GTTTTTGCTG	600
CATTACTTAC	AGGTCAACTC	TACCATATCA	GTCAGGGTGG	ATAATTTCCA	GTATGTGGAT	660
ACAAACACTT	TCCCTCTTGA	TAATGTGCTA	TCCGTCTTCT	TATATAGTAG	CTCAGACTGA	720

APPLICATION

FOR

UNITED STATES LETTERS PATENT

NOVEL EXPRESSION VECTORS CONTAINING ACCESSORY
MOLECULE LIGAND GENES AND THEIR USE FOR
IMMUNOMODULATION AND TREATMENT OF
MALIGNANCIES AND AUTOIMMUNE DISEASE

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231/003
Patent

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DESCRIPTION

NOVEL EXPRESSION VECTORS CONTAINING ACCESSORY MOLECULE
LIGAND GENES AND THEIR USE FOR IMMUNOMODULATION AND
TREATMENT OF MALIGNANCIES AND AUTOIMMUNE DISEASE

RELATED APPLICATION

This application claims priority to Kipps et al.,
NOVEL EXPRESSION VECTORS CONTAINING ACCESSORY MOLECULE
5 LIGAND GENES AND THEIR USE FOR IMMUNOMODULATION AND
TREATMENT OF MALIGNANCIES, United States Provisional
Application No. 60/132145, filed December 9, 1996, which
is incorporated herein by reference including drawings.

10

TECHNICAL FIELD OF THE INVENTION

The present invention relates to novel expression
vectors containing genes which encode an accessory
molecule ligand and the use of those vectors for
15 immunomodulation, improved vaccination protocols and the
treatment of malignancies and autoimmune diseases. More
particularly, this invention provides expression vectors
and methods for treating various neoplastic or malignant
cells, and expression vectors and methods for treating
20 autoimmune Disease. This invention also contemplates
the production and expression of accessory molecule
ligands with greater stability and enhanced function.

BACKGROUND OF THE INVENTION

25

Leukemias, lymphomas, carcinomas and other
malignancies are well known and described in, e.g.,
Harrison's Principles of Internal Medicine, Wilson et
al., eds., McGraw-Hill, New York, pp. 1599-1612. These

malignancies appear to have somehow escaped the immune system surveillance mechanisms that eliminate rapidly and continuously proliferating cells. The exact mechanism by which these malignancies escape the immune system surveillance is not known.

Some of these malignant immune system cells are malignant antigen presenting cells which do not function properly within the immune cascade. For example, neoplastic B cells cannot induce even weak allogeneic or autologous mixed lymphocyte reactions in vitro. Further evidence that malignancies survive due to the failure of the immune surveillance mechanism includes the increased frequency of such malignancies in immunocompromised individuals, such as allograft recipients and those receiving long-term immunosuppressant therapy. Further, the frequency of these malignancies is increased in patients having Acquired Immune Deficiency Syndrome (AIDS) and patients with primary immune deficiency syndromes, such as X-linked lymphoproliferative syndrome or Wiscott-Aldrich Syndrome (Thomas et al., Adv. Cancer Res. 57:329, 1991).

The immune system normally functions to eliminate malignant cells by recognizing the malignant cells as foreign cells and clearing those cells from the body. An immune reaction depends on both the immune system's antibody response and on the cellular immune response within a patient. More specifically, the cellular immune response which acts to recognize the malignant cells as foreign requires a number of different cells of the immune system and the interaction between those cells. An immune reaction begins with a T lymphocyte (T cell) which has on its cell surface the T cell receptor. The T cell also has the ability to express on its surface various accessory molecules which interact with accessory molecules on the B lymphocyte (B cell). When

the T cell receptor of the T cell specifically binds to a foreign antigen, such as a malignant cell, it becomes activated and expresses the accessory molecule ligand, CD40 ligand on its cell surface. The accessory cell molecule ligand is only present on the activated T cells for a short period of time and is rapidly removed from the cell surface. After the accessory cells molecule ligand is removed from the surface of the activated T cell, its ability to bind to B cells via the accessory molecule ligand is destroyed.

When present on the surface of an activated T cell, the accessory cell ligand can specifically bind to the accessory cell molecule present on the B cell. This specific T-B cell interaction causes the B and T cell to express costimulatory surface accessory molecule and cytokines which result in an immune activation which lead to cytolytic T cells which specifically kill and remove the malignant cell from the body.

The interaction with an activated T cell is not solely limited to B cells but rather can be carried out by any cell which is able to present antigen to the T cell (an antigen presenting cell). These cells include B lymphocyte, macrophages, dendritic cells, monocytes, Langerhans cells, interdigitating cells, follicular dendritic cells or Kupffer cells. These cells all are known to have various accessory molecules on the cell surface which allow them to interact with other cells of the immune system. For example, these antigen presenting cells all have the accessory molecule CD40 on their cell surface. The presence of these accessory molecules allows these antigen presenting cells to specifically bind to complimentary accessory molecule ligand and thus directly interact with other immune cells.

A large number of accessory molecule ligands are members of the tumor necrosis factor superfamily. (Fanslow et al., Sem. Immun., 6:267-268 (1994)). The genes for a number of these accessory molecule ligands have been cloned and identified. These accessory molecule ligand genes encode accessory molecules which all have the configuration of Type II membrane proteins and exhibit varying degrees of homology with other accessory molecule ligand genes. For example, the accessory molecule ligand genes encoding both murine CD40 ligand and human CD40 ligand have been isolated. See, Armitage et al., Nature, 357:80-82 (1992) and Hollenbaugh et al., EMBO J., 11:4313-4321 (1992).

CD40 and its ligand, CD40 ligand are critical components of a normal immune response. CD40 mediated signals induce immune lymphocytes to proliferate and differentiate and become potent antigen presenting cells. Malignant or neoplastic B cells are poor antigen presenter cells and are unable to stimulate a vigorous allogeneic mixed lymphocyte reaction. Successful cross linking of CD40 molecules on immune cells results in a strong allogeneic mixed lymphocyte reaction suggesting a strong immune reaction. Various soluble CD40 ligands or antibodies specific for CD40 have been used to potentially cross link CD40. These soluble CD40 ligands and CD40-specific antibodies are not optimal for cross linking the CD40 molecules on antigen presenting cells and do not work as effectively as CD40 ligand expressed on a cell membrane to produce strong stimulation of antigen presenting cells. These methods are also difficult to implement because large amounts of CD40 ligand constructs or antibodies must be isolated which is difficult and time-consuming work. Other strategies to utilize CD40 ligand in solution or as a membrane bound molecule including transformation of fibroblasts

with CD40 ligand to produce cultured cells which are then used to present antigen are not amenable to in vivo human clinical protocols.

CD95 (Fas) interaction with its ligand (Fas-ligand, or FasL) functions to limit the duration of the immune response and/or life-span of activated lymphocytes. Apoptosis induced by Fas-FasL binding serves to clear activated self-reactive lymphocytes. Problems caused by altering this pathway have been demonstrated in animals with defects in Fas<->Fas-ligand interactions. Mice having mutations, which inactivate CD95 or FasL, develop numerous disorders including autoimmune pathology resembling that seen in patients with rheumatoid arthritis (RA) or systemic lupus. Zhang, et al., in J. Clin. Invest. 100:1951-1957 (1997) show that injection of FasL-expressing virus, into the joints of mice with collagen-induced-arthritis, results in apoptosis of synovial cells and relief of arthritis symptoms. Expression of Fas ligand allows clearance of activated cells which play a role in the pathogenesis of autoimmune disease. Therefore, a gene therapy strategy for introducing FasL into the joints of rheumatoid arthritis patients could function to improve disease pathology by leading to destruction of the infiltrating mononuclear cells.

Administration of soluble accessory molecules and accessory molecule ligands has been shown to trigger or to be associated with adverse physiological effects. For example, treatment of mice, having wild-type CD40-receptor expression, with soluble CD40L-CD8 fusion protein resulted in a pulmonary inflammatory response. This was not observed in mice in which the gene for the CD40 receptor had been knocked out. These experiments, described in Wiley, J.A. et al., Journal of Immunology 158:2932-2938 (1997), support in vitro data which

suggest that CD40 ligation can result in inflammatory responses.

Direct administration of purified recombinant soluble Tumor Necrosis Factor (either α or β) results in shock and tissue injury, as described in Tracey, K. J., and A. Cerami, Annu. Rev. Med. 45:491-503 (1994). Within minutes after acute intravenous or intra-arterial administration of TNF, a syndrome of shock, tissue injury, capillary leakage syndrome, hypoxia, pulmonary edema, and multiple organ failure associated with a high mortality ensues. Chronic low dose of TNF causes anorexia, weight loss, dehydration and depletion of whole-body protein and lipid.

Soluble Fas ligand and receptor have also been shown to be associated with tissue damage and other adverse effects. CD95, the Fas receptor, is a mediator of apoptosis. Fas ligand induces apoptosis by binding to Fas receptor. As shown in Galle, P.R., et al., J. Exp. Med. 182:1223-1230 (1995) administering an agonistic anti-Fas antibody resulted in liver damage to mice. Mice injected intraperitoneally with the agonistic antibody died within several hours, and analyses revealed that severe liver damage by apoptosis was the most likely cause of death.

The role of soluble Fas ligand (FasL), in the pathogenesis of systemic tissue injury in aggressive lymphoma is described in Sato, K. et al., British Journal of Haematology, 94:379-382 (1996). The findings presented in this report indicate that soluble FasL is directly associated with the pathogenesis of liver injury and pancytopenia.

CD27, the receptor for the accessory molecule ligand, CD70, was shown, in a report written by van Oers, et al., in Blood 82:3430-3436 (1993), to be associated with B cell malignancies.

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The above findings all contraindicate the administration of soluble accessory molecule ligands, highlighting the need for therapies that increase the levels of these molecules without resulting in an elevation of their soluble forms.

Despite the wealth of information regarding accessory molecule ligand genes and their expression on the surface of various immune cells, the exact mechanism by which the accessory molecule ligand genes are regulated on antigen presenting cells is not yet known. Without specific knowledge of the regulation of expression of accessory molecule ligand genes on these antigen presenting cells, altering the immune response by varying expression of an accessory molecule ligand gene has to date not been possible. Without any specific knowledge as to how to regulate the expression of an accessory molecule ligand gene on an antigen presenting cell, it is not possible to alter the immune response towards malignant cells. Thus, there was a need for a method of increasing the expression of an accessory molecule ligand gene on normal and malignant cells including antigen presenting cells.

Further, without the ability to regulate the expression of accessory molecule ligands, it is not possible to alter the immune clearance of these cells.

SUMMARY OF THE INVENTION

The present invention fills these needs by providing novel expression vectors containing accessory molecule ligand genes and methods for introducing those genes into normal and malignant antigen presenting cells thereby allowing the alteration of an immune response, the treatment of autoimmune diseases and the treatment of various neoplasias. This invention provides vectors,

including gene therapy vectors which contain accessory molecule ligand genes. These vectors also contain the additional genetic elements, such as promoters, enhancers, polyadenylation signals (3' ends), which
5 allow that vector to be successfully placed within the cell and to direct the expression of the accessory molecule ligand gene in a cell. Such gene therapy vectors are capable of transforming animal cells directly and thereby introducing the accessory molecule
10 ligand gene into the cells of that animal in a form which can be utilized to produce accessory molecule ligands within that cell.

In other aspects of the present invention, the function of an accessory molecule ligand is modified by
15 altering the half life of the molecule on the cell surface or by changing the level of expression of that molecule on the cell surface. In preferred embodiments, the present invention provides accessory molecule ligands which are modified to improve the stability of
20 such accessory molecule ligands on the cell surface. Such increased stability may be accomplished using any of the disclosed methods of molecules described in this application, including chimeric molecules and molecules into which mutations have been introduced at least one
25 location. The present invention also contemplates increasing the expression of such a molecule.

The present invention also provides gene therapy vectors containing the accessory molecule ligand genes which are chimeric in that portions of the gene are
30 derived from two separate accessory molecule ligands which may or may not be from different species. The accessory molecule ligand genes of the present invention include genes which encode molecules of the tumor necrosis factor (TNF) family. The molecules which make
35 up the TNF family include TNF_{α} , TNF_{β} , CD40 ligand, Fas

ligand, CD70, CD30 ligand, 41BB ligand (4-1BBL), nerve growth factor and TNF-related apoptosis inducing ligand (TRAIL). In some embodiments of the present invention, the chimeric accessory molecule ligand genes of the present invention contain at least a portion of a murine accessory molecule ligand gene together with portions of accessory molecule ligand genes derived from either mouse, humans or other species. Some preferred embodiments of the present invention utilize murine CD40 ligand genes and chimeric CD40 ligand genes containing at least a segment of the murine CD40 ligand gene together with at least a segment of the human CD40 ligand gene. The present invention contemplates chimeric accessory molecule ligand genes wherein segments from the accessory molecule ligand gene of one species have been interchanged with segments from a second accessory molecule ligand gene which may optionally be from a different species. For example, in one preferred embodiment, the murine CD40 ligand gene transmembrane and cytoplasmic domains have been attached to the extracellular domains of human CD40 ligand gene.

The present invention contemplates gene therapy vectors which are capable of directly infecting the human, mammal, insect, or other cell. The use of such gene therapy vectors greatly simplifies inserting an accessory molecule ligand gene into those cells. The contemplated gene therapy vectors may be used in vivo or in vitro to infect the desired cell and are particularly useful for infecting malignant cells to effect sustained high-level expression of a physiologic ligand.

The present invention also contemplates animal, mammal, and human cells containing a gene therapy vector which includes an accessory molecule ligand gene and sufficient genetic information to express that accessory molecule ligand within that cell. In preferred

embodiments, the present invention also contemplates human neoplastic antigen presenting cells which contain the gene therapy vectors of the present invention or contain an accessory molecule ligand gene together with
5 a promoter and 3' end region.

The present invention also contemplates human cells and human neoplastic cells containing a gene therapy vector which includes a chimeric accessory molecule ligand gene. The present invention also contemplates
10 bacterial cells or animal cells containing accessory molecule ligand genes, chimeric accessory molecule ligand genes, murine accessory molecule ligand genes, human accessory molecule ligand genes, the gene therapy vectors of the present invention, the vectors of the
15 present invention, and a chimeric accessory molecule ligand gene together with a heterologous promoter, enhancer or polyadenylation sequence.

The present invention also contemplates methods of altering immune response within a human patient or the
20 immunoreactivity of human cells in vivo by introducing a gene which encodes an accessory molecule ligand gene into the human cells so that that accessory molecule ligand is expressed on the surface of those human cells. This method includes the introduction of the accessory
25 molecule ligand gene as part of a gene therapy vector or in association with a heterologous or native promoter, enhancer or polyadenylation signal. Some preferred embodiments of the present invention utilize introduction of Fas ligand genes and chimeric Fas ligand
30 genes, constructed as contemplated above for CD40, into human cells to alter their immunoreactivity. The present invention also includes methods in which such accessory molecule ligand genes are inserted into cells which have the accessory molecule to which the accessory

molecule ligand binds on the surface of the cell into which the accessory molecule ligand gene.

5 The present methods of altering immunoreactivity are applicable to all types of human, animal, and murine cells including human neoplastic cells such as human lymphomas, leukemias and other malignancies. In preferred embodiments, this method is used to introduce the gene encoding the accessory molecule ligand into potential antigen presenting cells of a human patient or
10 cell which can stimulate bystander antigen presenting cells. Such antigen presenting cells include monocytes, macrophages, B cells, Langerhans cells, interdigitating cells, follicular dendritic cells, Kupffer cells, and the like. The various antigen presenting cells may be present as part of a known malignancy in a human patient such as leukemias, lymphomas, acute monocytic leukemia (AML), chronic lymphocytic leukemia (CLL), acute myelomonocytic leukemia (AMML), chronic myelogenous or chronic myelomonocytic leukemia (CMML) and thus would
20 include all tumors of any cell capable of presenting antigen to the human or animal immune system or are capable of stimulating bystander antigen presenting cells. The present invention also contemplates modulating the immune system by introducing genes encoding an accessory molecule ligand gene of the present invention into any number of different cells found in a patient, including muscle cells, skin cells, stromal cells, connective tissue cells, fibroblasts and the like.

30 The present invention also contemplates methods of treating neoplasias in either a human patient or an animal patient. In one preferred embodiment, the method comprises isolating the neoplastic cells from the human or animal patient and inserting into those isolated
35 cells the gene which encodes the chimeric accessory

5 molecule ligand or the accessory molecule ligand so that that molecule is expressed on the cell surface of those neoplastic cells or other somatic cells. The neoplastic cells are then infused back into the human or animal patient and may then participate in an enhanced immune response.

10 The present invention also contemplates the co-infection or co-introduction of the accessory molecule ligand gene together with a gene which encodes a tumor or carcinoma specific antigen. This combination of molecules are then expressed on the surface of the neoplastic cells and when those cells are introduced into the patient lead to the rapid immune response resulting in the destruction of those cells.

15 The present methods also include directly introducing the gene therapy vector or other vector carrying the accessory molecule ligand gene directly into the tumor or tumor bed of a patient. Upon entering the tumor bed of the patient, the gene therapy vector or other vector enter the cells present in the tumor or tumor bed and then express the accessory molecule ligand gene on the surface of those cells. These cells then are able to participate fully in the human immune or animal immune response.

25 The present invention also contemplates methods of augmenting an immune response to a vaccine. The present method of vaccinating an animal against a predetermined organism or antigen by administering to that animal a vaccine which has a genetic vector containing an accessory molecule ligand gene. Other embodiments of the present invention include vaccinating an animal by administering two separate genetic vectors, one containing the antigens from the organism to which immunity is desired by isolating the cells of the target animal and contacting with those cells a vector encoding

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at least one antigen from a predetermined organism so that the antigen is expressed by the cells and also contacting those cells with a different vector which expresses the accessory molecule ligand gene on the
5 surface of the animal's antigen presenting cells. Together these two separate vectors produce a vaccination which is much stronger and of longer duration than is vaccination with antigen alone.

The present methods of vaccination are applicable
10 to vaccinations designed to produce immunity against a virus, a cell, a bacteria, any protein or a fungus. The present methods are also applicable to immunization against various carcinomas and neoplasias. In these embodiments, the tumor antigen against which immunity is
15 desired is introduced into the animal together with the genetic vector containing the accessory molecule ligand gene.

The present invention also contemplates methods of treating arthritis utilizing a gene therapy vector
20 encoding an accessory molecule ligand. Of particular interest for use with arthritis is the Fas ligand molecule in which the expression of Fas ligand activity has been increased in the joint and/or the stability of the Fas ligand activity on cells within the joint
25 enhanced. In other embodiments, the present invention contemplated methods of treating arthritis utilizing chimeric accessory molecule ligands and chimeric accessory molecule ligand genes. The present invention also contemplates both ex vivo therapy and in vivo
30 therapy of arthritis utilizing the expression vectors of the present invention together with the Fas ligand and modified versions of that molecule including chimeric molecules.

35

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1. Figure 1 is a diagram showing a number of accessory molecule ligand genes and Domains I-IV of those genes as deduced from sequence data.

Figure 2. Figure 2 is a diagram showing example chimeric accessory molecule ligand genes. The domains derived from the murine accessory module are shown shaded.

Figure 3. Figure 3 shows the amount of either mouse or human CD40 ligand found on the surface of Hela or CLL cells infected with gene therapy vectors containing the genes encoding these molecules. Figure 3A shows uninfected Hela cells (shaded) and Hela cells infected with a gene therapy vector encoding murine CD40 ligand. Figure 3B shows uninfected Hela cells (shaded) and Hela cells infected with a gene therapy vector encoding human CD40 ligand. Figure 3C shows uninfected CLL cells (shaded) and CLL cells infected with a gene therapy vector encoding murine CD40 ligand. Figure 3D shows uninfected CLL cells (shaded) and CLL cells infected with a gene therapy vector encoding human CD40 ligand.

Figure 4. Figure 4 shows histograms of the increased expression of CD54 (Figure 4B) and CD80 (Figure 4D) on CLL cells into which a gene therapy vector containing the accessory molecule ligand gene (murine CD40 ligand gene) has been introduced. The shaded graph indicates control stain in FACS analysis and the open graph indicates staining with monoclonal antibodies immunospecific for either CD54 (Figures 4A and 4B) or CD80 (Figures 4C and 4D).

Figure 5. Figure 5 shows the cell proliferation as measured by ³H-TdR incorporation of allogeneic T cells in response to various stimulation regimes. The CLL cells

containing a gene therapy vector expressing an accessory molecule ligand gene (the murine CD40 ligand gene) were introduced, stimulating allogeneic T cells to proliferate.

5 Figure 6. Figure 6 shows the production of gamma interferon (IFN γ) by allogeneic T cells stimulated with CLL cells containing an accessory molecule ligand gene.

10 Figure 7. Figure 7 shows the treatment of a neoplasia in an animal using a gene therapy vector containing an accessory molecule ligand gene of the present invention. The open squares show mice immunized with neoplastic cell not expressing an accessory molecule ligand of the present invention. Mice immunized with neoplastic cells expressing an accessory molecule ligand of the present invention are shown as the horizontal line at the top of the Figure and show no morbidity.

15 Figure 8. Figure 8 shows the production levels and stabilities of CD40 ligand and CD40 ligand transcript in CLL (upper graph) and normal blood mononuclear cells (lower graph).

20 Figure 9. Figure 9 shows the time course of transgene expression in CLL B cells infected with the accessory molecule ligand (CD40 ligand). The MFIR (mean fluorescence intensity ratio), comparing the fluorescence intensity of CD19⁺ CLL cells stained with PE-labeled CD40 ligand versus the same stained with a PE-labeled isotype control mAb at each time point, are represented by the closed circles connected by solid lines according to the scale provided on the left-hand ordinate.

25 Figure 10. Figure 10 shows changes in surface antigen phenotype of CLL B cells infected with a gene therapy vector containing an accessory molecule ligand, CD40 ligand. Shaded histograms represent staining of

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uninfected CLL cells (thin lines) stained with nonspecific control antibody, open histograms drawn with thin lines represent uninfected CLL cells stained with FITC-conjugated specific mAb, and open histograms drawn with thick lines (labeled CD154-CLL) represent CLL cells infected with the accessory molecule ligand gene therapy vector and stained with FITC-conjugated specific mAb.

Figure 11. Figure 11 shows levels of CD27 produced in CLL cells infected with a gene therapy vector containing an accessory molecule ligand. Figure 11A shows that CD40L-infected CLL (CD154-CLL) cells express reduced levels of surface CD27. Open histograms represent staining of non-infected CLL cells (thin lines) or infected CLL (thick lines) with FITC-conjugated α CD27 mAb, respectively. Figure 11B shows production of soluble form of CD27 by CLL B cells.

Figure 12. Figure 12 shows allogeneic T cell responses induced by CLL cells infected with a gene therapy vector containing an accessory molecule ligand (CD40 ligand, also called CD154). Figure 12A indicates the concentration of IFN γ in the supernatants after stimulation of allogeneic T cells with CLL cells containing the accessory molecule ligand. Figure 12B shows cell proliferation, as assessed by incorporation of 3 H-thymidine. Figures 12C and 12D show secondary allogeneic T cell responses induced by CLL containing the accessory molecule ligand.

Figure 13. Figure 13 depicts autologous T cell responses induced by CLL B cells containing the accessory molecule ligand, CD40 ligand or CD154, and controls. Figure 13A shows incorporation of 3 H-thymidine by autologous T cells co-cultured with the CLL cells. Figure 13B shows the levels of human IFN γ produced by autologous T cells co-cultured with the CLL cells. In Figure 13C, the CTL activities of autologous T cells

induced by CLL B cells containing the accessory molecule ligand are graphed.

Figure 14. Figure 14 shows specificity of CTL for autologous CLL B cells. IFN γ concentration was assessed in the supernatants after 48 h of culture (Figure 14A), and cytolytic activity was assessed at 3 h of culture (Figure 14B). In Figure 14C, mAb were added to the autologous leukemia target cells prior to the CTL assay.

Figure 15. Figure 15 shows that intercellular stimulation plays a role in production of the phenotypic changes observed in CLL cells expressing the accessory molecule ligand. In Figure 15A, the effect of culture density on the induced expression of CD54 and CD80 following infection with a gene therapy vector containing the accessory molecule ligand (CD40 ligand, CD154) is shown. Shaded histograms represent staining of leukemia B cells with a FITC-conjugated isotype control mAb. Open histograms represent CD154-CLL B cells, cultured at high or low density (indicated by arrows), and stained with a FITC-conjugated mAb specific for CD54 or CD80. Figure 15B shows inhibition of CD154-CLL cell activation by anti-CD154 mAb. Figures 15C and 15D depict expression of immune accessory molecules on bystander non-infected CLL B cells induced by CLL cells expressing the accessory molecule ligand. Shaded histograms represent staining with PE-conjugated isotype control mAb.

Figure 16. Figure 16 shows that the vector encoding an accessory molecule ligand enhances immunization against β -gal in mice. Figure 16A shows that mice that received intramuscular injections of the pCD40L vector produced significantly more antibodies to β -gal than did mice injected with either the non-modified pcDNA3 vector or pCD40L. Figure 16B, ELISA analyses of serial dilutions of sera collected at d28, shows that mice co-

injected with placZ and pCD40L had an eight-fold higher mean titer of anti- β -gal antibodies at d28 than mice treated with placZ + pcDNA3.

Figure 17. Figure 17 shows analysis of the IgG₁ and IgG_{2a} immune responses to intramuscular plasmid DNA immunizations with and without a vector, pCD40L, encoding an accessory molecule ligand. IgG_{2a} anti- β -gal antibodies predominated over IgG₁ subclass antibodies in the sera of mice injected with either placZ and pcDNA3 or placZ and pCD40L. In contrast, BALB/c mice injected with β -gal protein developed predominantly IgG₁ anti- β -gal antibodies, and no detectable IgG_{2a} anti- β -gal antibodies.

Figure 18. Figure 18 shows the comparison between injection of mice with a vector, pCD40L, encoding an accessory molecule ligand, at the same and different sites as placZ. Adjuvant effect of pCD40L requires co-injection with placZ at the same site.

Figure 19. Figure 19 shows that co-injection into dermis of a vector encoding an accessory molecule ligand, pCD40L, with placZ enhances the IgG anti- β -gal response in BALB/c mice.

Figure 20. Figure 20 shows that a vector encoding an accessory molecule ligand, pCD40L, enhances the ability of placZ to induce CTL specific for syngeneic β -gal-expressing target cells. Splenocyte effector cells, taken from mice which had received injections of placZ and pCD40L, specifically lysed significantly more cells than did splenocytes from mice that received control injections.

Figure 21. Figure 21 shows downmodulation of human CD40L, but not murine CD40L, in lung tumor cell lines that express CD40.

Figure 22. Figure 22A shows that CD40 binding induces enhanced expression of the tumor cell surface

markers CD95 (Fas), CD54 (ICAM-1), and MHC-I, in lung tumor cell lines. Figure 22B shows downmodulation of human CD40L by CD40-positive tumor cells.

Figure 23. Figure 23 shows the inhibition of Fas
5 ligand expression by lymphocytes in the presence of RA synovial fluid.

Figure 24. Figure 24 shows an outline for a clinical trial of an accessory molecule ligand (CD40L) gene therapy treatment for B cell CLL.

10 Figure 25. Figure 25 shows a sequence line-up of human Fas ligand with human Fas ligand in which Domain III is replaced by Domain III of murine Fas ligand. The top protein sequence is native human Fas ligand. Domain III is underlined with the dotted line. The double
15 underline indicates a putative MMP cleavage site. The bottom protein sequence is that of chimeric human-mouse Fas ligand. Domain III of the mouse Fas ligand (underlined with dotted line) is substituted for Domain III of human Fas ligand. The numbers correspond to the
20 amino acid sequence number using 1 for the start of the polypeptide sequence. The number of the first nucleotide base for the codon encoding the amino acid is $1+3x(n-1)$, where n is the amino acid sequence number.

Figure 26. Figure 26 shows a sequence line-up of
25 human Fas ligand with human Fas ligand in which Domain III has been replaced with Domain III of human CD70. The top protein sequence is native human Fas ligand, and the bottom sequence is that of chimeric Fas ligand, in which Domain III of human CD70 has been substituted for
30 Fas Domain III. Other markings are used similarly as in Figure 25.

Figure 27. Figure 27 shows a sequence line-up of human Fas ligand with human Fas ligand in which Domain I
35 has been replaced with Domain III of human CD70. The top protein is native human Fas ligand, and the bottom

protein sequence is that of chimeric Fas ligand, in which Domain III has been replaced with Domain I of human CD70. Other markings are used similarly as in Figure 25.

5 Figure 28. Figure 28 shows the amino acids around and at known matrix metalloproteinase (MMP) cleavage sites, as described in Smith, M.M. et al., Journal of Biol. Chem. 270:6440-6449 (95) and Nagase, H., and G.B. Fields, Biopolymers (Peptide Science) 40:399-416 (96).
10 The cleavage site is indicated with an arrow.

DETAILED DESCRIPTION OF THE INVENTION

15 All references cited herein are hereby incorporated in their entirety by reference.

I. Definitions

20 An "accessory molecule ligand gene" is a gene which encodes all or part of an accessory molecule ligand. The gene comprises at least the nucleotide sequence required to encode the functional portion of an accessory molecule ligand. The gene may optionally include such genetic elements as promoters, enhancers
25 and 3' ends. The accessory molecule ligand gene is derived from a ligand which is a member of the tumor necrosis factor (TNF) family, including CD40 ligand, Fas ligand, CD70, TNF α , TNF β , CD30 ligand, 4-1BB ligand (4-1BBL), nerve growth factor and TNF-related apoptosis
30 inducing ligand (TRAIL). As used herein, the term "accessory molecule ligand gene" includes chimeric accessory molecule ligand genes as defined below.

35 As used herein, the term "malignant cells or neoplastic cells," is defined to mean malignant or cancerous cells which are found in a human patient or an

animal. Preferred types of malignant or neoplastic cells include any malignant antigen-presenting cell. In some preferred embodiments, these malignant antigen presenting cells have at least low levels of CD40 present on the cell surface.

As used herein, the term "neoplastic human cells" is defined to mean human cells which are neoplastic including but not limited to antigen presenting cells, any neoplastic cell which may function as an antigen presenting cell or function to facilitate antigen presentation, neoplastic monocytes, neoplastic macrophages, neoplastic B cells, neoplastic dendritic cells, neoplastic Langerhans cells, neoplastic interdigitating cells, neoplastic follicular dendritic cells, or neoplastic Kupffer cells and the like. The definition of neoplastic human cells includes those cells which are associated with neoplastic cells in the tumor bed of human patients. Typically, the neoplastic human cells are either leukemias, lymphomas, AML, ALL, AMML, CML, CMML, CLL other tumors of antigen presenting cells or breast, ovarian or lung neoplastic cells. It is also contemplated that the accessory molecule ligand genes or chimeric accessory molecule ligand genes of the present invention may be inserted into somatic cells. These somatic cells can be created by a genetic engineering process which has introduced into those cells genes which encode molecules which render those cells capable of presenting antigen to the immune system.

As used herein, the term "chimeric gene" is defined to mean a gene in which part of the gene is derived from a second different gene and combined with the first gene so that at least a portion of each gene is present in the resulting chimeric gene. A gene may be chimeric if any portion of the sequence which encodes the resulting

protein is derived from a second and different gene. Typical chimeric genes include genes in which specific functional domains from one gene have been transferred to a second gene and replace the analogous domains of that second gene. For example, the resulting chimeric gene may have one domain derived from a murine gene and several domains derived from a human gene. These domains may range in size from 5 amino acids to several hundred amino acids. Other examples of chimeric accessory molecule ligand genes include genes which contain nucleotides encoding amino acids not found in any naturally occurring accessory molecule ligand gene. Examples of chimeric genes and potential various combinations of domains are numerous and one of skill in the art will understand that no limit is placed on the amount of one gene that must be present in a second gene to render it chimeric.

As used herein, the term "murine CD40 ligand gene" is defined to mean an accessory molecule ligand gene which is derived from a murine CD40 ligand gene. Examples of such murine CD40 ligand genes include the gene isolated by Armitage et al., Nature, 357:80-82 (1992) and other genes derived from murine origin which hybridize to the gene described by Armitage et al. under low stringency hybridization conditions.

As used herein, the term "vector or genetic vector" is defined to mean a nucleic acid which is capable of replicating itself within an organism such as a bacterium or animal cell. Typical genetic vectors include the plasmids commonly used in recombinant DNA technology and various viruses capable of replicating within bacterial or animal cells. Preferred types of genetic vectors includes plasmids, phages, viruses, retroviruses, and the like.

As used herein, the term "gene therapy vector" is defined to mean a genetic vector which is capable of directly infecting cells within an animal, such as a human patient. A number of gene therapy vectors have been described in the literature, and include, the gene therapy vector described in Cantwell et al., Blood, In Press (1996) entitled "Adenovirus Vector Infection of Chronic Lymphocytic Leukemia B Cells." Such vectors have been described for example by Woll, P. J. and I. R. Hart, Ann. Oncol., 6 Suppl 1:73 (1995); Smith, K. T., A. J. Shepherd, J. E. Boyd, and G. M. Lees, Gene Ther., 3:190 (1996); Cooper, M. J., Semin. Oncol., 23:172 (1996); Shaughnessy, E., D. Lu, S. Chatterjee, and K. K. Wong, Semin. Oncol., 23:159 (1996); Glorioso, J. C., N. A. DeLuca, and D. J. Fink, Annu. Rev. Microbiol., 49:675 (1995); Flotte, T. R. and B. J. Carter, Gene Ther., 2:357 (1995); Randrianarison-Jewtougoff, V. and M. Perricaudet, Biologicals., 23:145 (1995); Kohn, D. B., Curr. Opin. Pediatr., 7:56 (1995); Vile, R. G. and S. J. Russell, Br. Med. Bull., 51:12 (1995); Russell, S. J., Semin. Cancer Biol., 5:437 (1994); and Ali, M., N. R. Lemoine, and C. J. Ring, Gene Ther., 1:367 (1994). All references cited herein are hereby incorporated by reference.

II. Genetic Vectors and Constructs Containing an Accessory Molecule Ligand Gene

A. Accessory Molecule Ligand Genes

In one embodiment of the present invention, preferred gene therapy vectors contain an accessory molecule ligand gene. This accessory molecule ligand gene may be derived from any source and may include molecules which are man-made and do not appear in

nature. The present invention contemplates accessory molecule ligand genes which are derived from the genes encoding molecules within the tumor necrosis family (TNF) which includes the genes encoding: murine CD40
5 ligand, human CD40 ligand, Fas ligand, TNF_α , TNF_β , CD30 ligand, 4-1BB ligand, nerve growth factor, CD70, TNF-related apoptosis inducing ligand (TRAIL) and chimeric accessory molecule ligands. The nucleotide sequence of one accessory molecule ligand, the sequence of at least
10 one form of the murine CD40 ligand gene, has been determined and is listed as SEQ ID NO: 1. The present invention contemplates the use of any accessory molecule ligand gene which is homologous to the sequence present in SEQ ID NO: 1, and thus hybridizes to this sequence at
15 low stringency hybridization conditions. One of skill in the art will understand that accessory molecule ligand genes, including murine CD40 ligand gene, useful in the present invention may be isolated from various different murine strains.

20 The nucleotide sequence of a human CD40 ligand gene has been determined and is shown as SEQ ID NO: 2. The present invention contemplates the use of any accessory molecule ligand gene which is homologous to SEQ ID NO: 2, and thus hybridizes to this sequence at low
25 stringency conditions. One of ordinary skill in the art will understand that the accessory molecule ligand genes, including the human CD40 ligand genes, useful in the present invention, may vary depending on the individual from which the gene is isolated and such
30 variations may prove useful in producing unique accessory molecule ligand genes. The present invention contemplates the use of the domains, sub-domains, amino acid or nucleotide sequence of the human CD40 ligand and/or human CD40 ligand gene as part of a chimeric

accessory molecule ligand or chimeric accessory molecule ligand gene.

The nucleotide sequence of a bovine CD40 ligand gene has been determined and is shown as SEQ ID NO: 8.

5 The present invention contemplates the use of any accessory molecule ligand gene which is homologous to SEQ ID NO: 8, and thus hybridizes to the sequence at low stringency conditions. One of ordinary skill in the art will understand that the accessory molecule ligand
10 genes, including the bovine CD40 ligand genes, may vary depending on the individual animal from which the gene is isolated and that such variations may prove useful in producing unique accessory molecule ligand genes.

The nucleotide sequence of human TNF_{α} and human TNF_{β}
15 have been determined and are shown as SEQ ID NOS: 9 and 10, respectively. The present invention contemplates the use of any accessory molecule ligand gene which is homologous to either human TNF_{α} or human TNF_{β} (SEQ ID NOS: 9 and 10, respectively), and thus hybridizes to
20 these sequences at low stringency conditions. The accessory molecule ligand genes useful in the present invention, including the human TNF_{α} and TNF_{β} genes, may vary depending on the particular individual from which the gene has been isolated and these variations may
25 prove useful in producing unique accessory molecule genes.

The nucleotide sequence of porcine TNF_{α} and TNF_{β} have been determined and are shown as SEQ ID NO: 11. The present invention contemplates the use of any
30 accessory molecule ligand gene which is homologous to either SEQ ID NO: 11, and thus would hybridize to these sequences at low stringency conditions. One of ordinary skill in the art will understand that the accessory molecule ligand genes, including the porcine TNF_{α} and
35 TNF_{β} genes, may vary depending on the particular animal

from which the gene is isolated and that such variation may prove useful in producing unique accessory molecule genes.

5 The nucleotide sequence of a murine TNF α gene has been determined and is shown as SEQ ID NO: 12. The present invention contemplates the use of any accessory molecule ligand gene which is homologous to SEQ ID NO: 12, and thus hybridizes to the sequence at low stringency conditions. One of ordinary skill in the art
10 will understand that the accessory molecule ligand genes, including the murine TNF α gene may vary depending on the individual from which the gene is isolated and that these variations may prove useful in producing unique accessory molecule genes.

15 The nucleotide sequence of human Fas ligand and murine (C57BL/6) Fas ligand have been determined and are shown as SEQ ID NOS: 13 and 14, respectively. The nucleotide sequence of murine Balb/c Fas ligand is shown as SEQ ID NO: 31. The present invention contemplates
20 the use of any accessory molecule ligand gene which is homologous to any of SEQ ID NOS: 13, 14, and 31, and thus hybridizes to the sequences at low stringency conditions. One of ordinary skill in the art will understand that the accessory molecule ligand genes,
25 including the human Fas ligand or murine Fas ligand genes may vary depending on the particular individual or animal from which the gene is isolated and that such variations may prove useful in producing any accessory molecule genes.

30 The nucleotide sequence of a human CD70 gene has been determined and is shown as SEQ ID NO: 15. The murine CD70 gene sequence has also been determined, and is shown as SEQ ID NO: 36 and was described by Tesselaar et. al, J. Immunol. 159:4959-65(1997). The present
35 invention contemplates the use of any accessory molecule

ligand gene which is homologous to SEQ ID NO: 15 or 36, and thus hybridizes to this sequence at low stringency conditions. One of ordinary skill in the art will understand that the accessory molecule ligand genes, including the human CD70 gene may vary depending on the individual from which the gene is isolated and that these variations may prove useful in producing unique accessory molecule ligand genes.

The nucleotide sequence of human CD30 ligand gene has been determined and is shown as SEQ ID NO: 16. The present invention contemplates the use of any accessory molecule ligand gene which is homologous to SEQ ID NO: 16, and thus hybridizes to this sequence at low stringency conditions. One of ordinary skill in the art will understand that the accessory molecule ligand genes, including the human CD30 ligand gene, may vary depending on the individual from which the gene is isolated and that such variations may prove useful in producing unique accessory molecule ligand genes.

The present invention also contemplates variations and variants of the nucleotide sequences of the accessory molecule ligand genes provided herein which are caused by alternative splicing of the messenger RNA. This alternative splicing of the messenger RNA inserts additional nucleotide sequences which may encode one or more optional amino acid segments which in turn allows the accessory molecule ligand encoded to have additional properties or functions.

The nucleotide sequence of a human and mouse 4-1BBL have been determined and are shown as SEQ ID NOS: 17 and 18, respectively. The present invention contemplates the use of any accessory molecule ligand gene which is homologous to either SEQ ID NOS: 17 or 18, and thus hybridizes to these sequences at low stringency conditions. One of ordinary skill in the art will

understand that accessory molecule ligand genes,
including the human 4-1BBL gene may vary depending on
the individual from which it is isolated and that such
variations may prove useful in producing unique
5 accessory molecule ligand genes.

The present invention also contemplates chimeric
accessory molecules containing any domain, sub-domain
portion, or amino acid sequence encoded by the following
genes: bovine TNF- α (SEQ ID NO: 21), murine CD40 ligand
10 (SEQ ID NO: 22), human nerve growth factor- β (SEQ ID NO:
23), murine nerve growth factor (SEQ ID NO: 24), rat Fas
ligand (SEQ ID NO: 25), human TNF-related apoptosis
inducing ligand (TRAIL) (SEQ ID NO: 41, Genbank
accession number U37518), murine TNF-related apoptosis
15 inducing ligand (TRAIL) (SEQ ID NO: 42, Genbank
accession number U37522), murine CD30-Ligand (SEQ ID NO:
43), human 4-1BBL (SEQ ID NO: 17), and murine 4-1BBL
(SEQ ID NOS: 44 and 18). The present invention also
contemplates chimeric accessory molecules which utilize
20 genes encoding amino acid sequences homologous to these
sequences.

The present invention contemplates chimeric
accessory molecule ligand genes which are comprised of a
nucleotide segment derived from one accessory molecule
25 ligand gene operatively linked to a nucleotide sequence
derived from a different accessory molecule ligand gene
or other gene.

For example, chimeric accessory molecule ligand
genes are contemplated which are comprised of a segment
30 of the murine CD40 ligand gene which has been
operatively linked to at least one other additional gene
segment derived from a different accessory molecule
ligand gene. The size of the particular segment derived
from the different accessory molecule ligand gene may
35 vary from a nucleotide sequence encoding a few amino

acids, a sub-domain of the accessory molecule ligand, a domain of the accessory molecule ligand or more than a domain of an accessory molecule ligand. Other chimeric accessory molecules of the present invention are

5 comprised of an accessory molecule ligand gene into which nucleotides encoding an amino acid segment which is not found as part of a naturally occurring accessory molecule ligand have been inserted. This amino acid segment may be artificially created or derived from a

10 protein found in nature. The chimeric accessory molecule ligand gene encodes a chimeric amino acid sequence and thus a chimeric accessory molecule ligand encoded may possess unique properties in addition to the properties found on the individual segments derived from

15 the different accessory molecule ligand genes. The chimeric accessory molecule ligand gene may encode an accessory molecule ligand which has properties derived from the accessory molecule ligand used to construct the chimeric gene.

20 Each of the accessory molecule ligand genes which are a member of the tumor necrosis factor family have a similar secondary structure consisting of a number of domains. This domain structure includes a first domain which is encoded by the 5' region of the accessory

25 molecule ligand gene. The second domain (Domain II) is the domain which contains the amino acids which span the cell membrane and is thus called the transmembrane domain. The third domain (Domain III) is the proximal extracellular domain and these amino acids are the amino

30 acids which are found proximal to the cellular membrane. The fourth domain (Domain IV), is encoded by the 3' end of the accessory molecule ligand gene and has been called the distal extracellular domain. The distal extracellular domain (Domain IV) generally makes up the

35 soluble form of the tumor necrosis factor family

molecule. Based on the x-ray crystal structure of human TNF, the predicted secondary structure of the accessory molecule, CD40 ligand has been deduced together with the domain structure of these molecules by M. Peitsch and C. Jongeneel, International Immunology, 5:233-238 (1993). The secondary structures of the other members of the tumor necrosis factor family were deduced using computer analysis together with comparison to the human TNF and CD40 ligand domain structure. In Table I, the domain boundaries of a number of accessory molecule ligand genes is shown. A diagram of these domains for a number of these accessory cell molecule ligands is shown in Figure 1. The assignments of the domain boundaries are approximate and one of ordinary skill in the art will understand that these boundaries may vary and yet still provide useful identification of domains.

TABLE I
DOMAIN STRUCTURE OF TUMOR NECROSIS
FACTOR FAMILY MOLECULES*

		Domain I (Cytoplasmic)	Domain II (Transmembrane)	Domain III (Proximal Extracellular)	Domain IV (Distal Extracellular)
5	Human CD40 Ligand	1-42	43-135	136-330	331-786
	Murine CD40 Ligand	1-42	43-135	136-327	328-783
10	Bovine CD40 Ligand	1-42	43-135	136-330	331-786
	Human TNF- α	1-87	88-168	169-228	229-699
	Murine TNF- α	1-87	88-168	169-237	238-705
	Porcine TNF- α	1-87	88-168	169-228	229-696
	Human TNF- β	1-39	40-129	130-153	154-615
15	Porcine TNF- β	1-39	40-126	127-150	151-612
	Human Fas Ligand	1-237	238-315	316-390	391-843
	Murine Fas Ligand	1-237	238-309	310-384	385-837
20	Human CD70	1-61	62-117	118-132	133-579
	Murine CD70	1-73	74-123	124-138	139-585
	Human CD30 Ligand	1-117	118-186	187-240	241-702
25	Murine CD30 Ligand	1-135	136-201	202-255	256-717
	Human 4-1BBL	1-69	70-174	175-210	211-762
30	Murine 4-1BBL	1-237	238-333	334-369	370-927
	Human TRAIL	1-39	40-117	118-375	376-843
35	Murine TRAIL	1-51	52-111	112-387	388-873

* The Domains above are identified by the nucleotide boundaries of each domain using the first nucleotide of the initial methionine of the cDNA as nucleotide number 1.

One of ordinary skill in the art will understand that typical chimeric accessory molecule genes would include genes produced by exchanging domains or sub-domain segments between, for example, a mouse CD40
5 ligand gene and a human CD40 ligand gene. For example, chimeric accessory molecule gene may be constructed by operatively linking Domain I of the human CD40 ligand gene to Domains II-IV of the murine CD40 ligand gene. One of ordinary skill in the art will understand the
10 variety of chimeric accessory molecule ligand genes which may be produced using the accessory molecules identified in Table I. The present invention also contemplates chimeric accessory molecules which are not shown in Table I but which are shown to have a similar
15 domain structure. Other chimeric genes are also contemplated in which smaller segments (sub-domain segments) are exchanged between, for example, a murine CD40 ligand gene and a human CD40 ligand gene or a second murine CD40 ligand gene. One of skill in the art
20 will understand that genes encoding accessory molecules will have at least gene segments which correspond to various functional segments of an accessory molecule ligand such as the murine CD40 ligand encoded by the murine CD40 ligand gene (SEQ ID NO: 1). It will also be
25 apparent to one of skill in the art that the nucleotide boundaries identified in Table I may vary considerably from those identified for the murine CD40 ligand gene (SEQ ID NO: 1) and still define domains which are useful in the present invention.

30 In one preferred embodiment, the chimeric accessory molecule ligand gene is comprised of the nucleotides encoding extracellular domains (Domains III and IV) of human CD40 ligand operatively linked to the nucleotides encoding transmembrane (Domain II) and the nucleotides
35 encoding cytoplasmic domain (Domain I) of the murine

CD40 ligand gene. Examples of such preferred chimeric accessory molecules are shown in Figure 2. An exemplary nucleotide sequence for such a gene is SEQ ID NO: 7. In other chimeric accessory molecule ligand genes of the present invention, the nucleotides encoding the extracellular domains (Domains III and IV) of the murine CD40 ligand gene may be operatively linked to nucleotides encoding the transmembrane (Domain II) and cytoplasmic domain (Domain I) of the human CD40 ligand gene. An exemplary nucleotide sequence for such a gene is SEQ ID NO: 3. In other preferred chimeric accessory molecule ligand genes of the present invention, the nucleotides encoding the extracellular domains (Domains III and IV) and transmembrane domain (Domain II) of human CD40 ligand are coupled to the nucleotides encoding cytoplasmic domain (Domain I) of murine CD40 ligand gene. An exemplary nucleotide sequence for such a gene is SEQ ID NO: 6. Other chimeric accessory molecule genes contemplated by the present invention comprise the nucleotides encoding the extracellular domains (Domains III and IV) and transmembrane domain (Domain I) of the murine CD40 ligand gene operatively linked to the nucleotides encoding cytoplasmic domain of the human CD40 ligand gene. An exemplary nucleotide sequence for such a gene is SEQ ID NO: 5. Other chimeric accessory molecule ligand genes are contemplated by the present invention in which the human CD40 ligand gene extracellular domains (Domain III and IV) is operatively linked to the murine CD40 ligand gene transmembrane domain (Domain I) which is operatively linked to the human CD40 ligand gene cytoplasmic domain (Domain I). An exemplary nucleotide sequence for such a gene is SEQ ID NO: 4.

One of ordinary skill in the art will understand that many more combinations which utilize domains or

other selected segments of any of the accessory molecule ligand genes including the human CD40 ligand genes and the mouse CD40 ligand genes are possible. Such additional chimeric accessory molecule genes would

5 include the following genes: chimeric accessory molecule genes in which the nucleotides encoding Domain I are selected from a particular accessory molecule ligand gene and operatively linked, either directly or by an additional nucleotide sequence to the nucleotides

10 encoding Domain II from a particular accessory molecule ligand gene. These domains then would be operatively linked either directly or by an additional nucleotide sequence to the nucleotides encoding Domain III from a particular accessory molecule ligand gene. This

15 molecule would then be operatively linked either directly or by an additional nucleotide sequence to the nucleotides encoding Domain IV of a particular accessory molecule ligand gene. The chimeric accessory molecule ligand gene constructed in this manner may have

20 additional nucleotides on either end or between domains which are useful to provide different amino acids in these positions. One of ordinary skill in the art will understand that these particular combinations are merely illustrations and that numerous other combinations could

25 be contemplated in which gene segments comprising nucleotides encoding less than the entire domain of an accessory molecule are exchanged between different accessory molecules.

The present invention also contemplates chimeric

30 accessory molecule ligand genes which are comprised of gene segments of mouse or human CD40 ligand in combination with gene segments derived from Fas ligand, TNF_{α} , TNF_{β} , CD70, CD30L, 4-1BBL, nerve growth factor or TNF-related apoptosis inducing ligand (TRAIL).

35 Particularly useful chimeric accessory molecule ligand

genes comprise at least one gene segment which is derived from a murine CD40 ligand gene together with gene segments or a gene segments derived from a different accessory molecule ligand gene.

5 The present invention also contemplates chimeric accessory molecule ligand genes in which the accessory molecules produced have been modified to remove amino acids within the chimeric accessory molecule that are used by post-translational mechanisms to regulate the
10 level of expression of the accessory molecule or accessory molecule protein on a particular cell. The sites removed from the chimeric accessory molecules or chimeric molecule may include amino acids or sites which make up protease cleavage sites including
15 metallothionine proteases, serine proteases and other proteases that recognize an amino acid sequence either specifically or nonspecifically. In particular preferred embodiments, amino acids in Domain III which make up potential or actual recognition site(s) used by
20 post-translational regulatory mechanisms have been modified or removed.

 The present invention also contemplates chimeric accessory molecule ligand genes in which the domains, subdomain fragments or other amino acid residues have
25 been taken from one accessory molecule ligand gene and moved into a second accessory molecule ligand gene from the same species. For example, in this particular embodiment, the human Domain I, and the human Domain II from the CD40 ligand molecule may be operatively linked
30 to the nucleotides encoding the human Domain III from, for example, the CD70 molecule which is in turn operatively linked to human Domain IV for the CD40 ligand molecule. This chimeric accessory molecule therefore contains human CD40L Domains I, II and IV and
35 human CD70 Domain III. An exemplary nucleotide sequence

for such a gene is SEQ ID NO: 19. One of ordinary skill in the art will understand that a number of such combinations using domains from the same species from different accessory molecule ligand genes may create a
5 number of chimeric accessory molecule genes which may all have specific activities and properties.

The present invention contemplates chimeric accessory molecule ligand genes in which the Domain III of a particular accessory molecule ligand gene has been
10 replaced with a Domain III from a different accessory molecule ligand gene. In one particularly preferred embodiment, the mouse Domain III has been used to replace the human Domain III in the CD40 ligand molecule. This chimeric accessory molecule therefore
15 contains the human CD40L Domain I, the human CD40L Domain II, mouse CD40L Domain III, and human CD40L Domain IV. An exemplary nucleotide sequence for such a gene is SEQ ID NO: 20.

The present invention also contemplates the use of
20 chimeric accessory molecules that contain man-made amino acid sequences inserted into or in place of a portion of a domain or other amino acid sequence of an accessory molecule gene. These man-made amino acid segments may be created by selecting any amino acid sequence that may
25 be used to give the accessory molecule a particular function or to remove another undesired function. These man-made amino acid segments are produced by inserting into the accessory molecule ligand gene or chimeric accessory molecule ligand gene the nucleotide sequences
30 required to encode those particular man-made amino acid segments in the desired positions. Further, the chimeric accessory molecule ligand genes may contain nucleotide segments which comprise sub-domain segments of other molecules or small segments in which amino
35 acids have been changed for a desired purpose. The use

of sub-domain nucleotide segments allows the introduction of short amino acid sequences derived from other molecules into chimeric accessory molecules of the present invention. The incorporation of such short sub-domain segments or amino acid changes into the accessory molecule ligand allows the introduction of desired or the removal of undesired features of that molecule.

The identification of domain structures within accessory cell molecules is well known in the art and generally requires the identification of cysteine residues within the accessory molecules and the subsequent mapping of disulfide bonds between various cysteine residues. The mapping of various sub-domain segments of an accessory molecule is well known in the art and involves analysis of the amino acid sequence of the accessory molecules and generally involves a comparison of the crystal structure of tissue necrosis factor with the use of predictive algorithms thereby producing a predicted structure of a chimeric accessory molecule or an accessory molecule. This predicted structure of these molecules can then be used to select various sub-domain portions of the molecule to be used to construct further chimeric accessory molecules. Examples of such mapping studies include the studies by M. Pitsch and C. V. Jongeneel, International Immunology, 5:233-238 (1993) and the analysis shown in Figure 1.

The present invention also contemplates accessory molecule ligand genes and chimeric accessory molecule ligand genes which are truncated and encode less than the full length of the amino acid sequence found in the native accessory molecule ligand. These truncations may alter the properties of the accessory molecule ligand gene but some identified activity is maintained. Such truncations may be made by removing a gene segment or gene segments from the accessory molecule gene and

typically would be performed by removing nucleotides encoding domains which are not directly involved in the binding of the accessory molecule ligand with its accessory molecule. These truncated accessory molecule
5 ligand genes or chimeric truncated accessory molecule ligand genes may contain further gene segments which encode amino acid segments or domains which replace the domains removed from that truncated accessory molecule gene. However, such replacement of the portions of the
10 accessory molecule removed by truncation is not necessary.

The chimeric accessory molecule genes of the present invention may be constructed using standard genetic engineering methods to operatively link a
15 particular nucleotide sequence from one accessory molecule ligand gene to a different nucleotide sequence derived from the same or different accessory molecule ligand gene. In addition, standard genetic engineering methods may be used to insert man-made nucleotide
20 sequences or sub-domain nucleotide sequences into the chimeric accessory molecule ligand gene. One of ordinary skill in the art will understand that various methods may be utilized to produce such chimeric accessory molecule genes. For example, a gene
25 conversion method known as "SOEN" may be used to produce a chimeric accessory molecule gene which contains nucleotide segments derived from different chimeric accessory molecules. The methods for using this gene conversion method are well known in the art and have
30 been described for example in Horton, R. M., Mol. Biotechnol., 3:93 (1995); Ali, S. A. and A. Steinkasserer, Biotechniques, 18:746 (1995); Vilardaga, J. P., E. Di Paolo, and A. Bollen, Biotechniques, 18:604 (1995); Majumder, K., F. A. Fattah, A. Selvapandiyar,
35 and R. K. Bhatnagar, PCR. Methods Appl., 4:212 (1995);

Boles, E. and T. Miosga, Curr. Genet. 28:197 (1995); Vallejo, A. N., R. J. Pogulis, and L. R. Pease, PCR. Methods Appl., 4:S123 (1994); Henkel, T. and P. A. Baeuerle, Anal. Biochem., 214:351 (1993); Tessier, D. C. and D. Y. Thomas, Biotechniques, 15:498 (1993); Morrison, H. G. and R. C. Desrosiers, Biotechniques, 14:454 (1993); Cadwell, R. C. and G. F. Joyce, PCR. Methods Appl., 2:28 (1992); and, Stappert, J., J. Wirsching, and R. Kemler, Nucleic Acids Res., 20:624 (1992). Alternatively, one of ordinary skill in the art will understand that site-directed mutagenesis may be used to introduce changes into a particular nucleotide sequence to directly produce or indirectly be used to produce a chimeric accessory molecule gene of the present invention. For example, the mutagen kit provided by BioRad Laboratories may be used together with the methods and protocols described within that kit to produce the desired changes in the nucleotide sequence. These methods were originally described by Kunkel, Proc. Natl. Acad. Sci. USA, 82:488-492 (1985) and Kunkel et al., Meth. Enzol. Mol., 154:367-382 (1987). By using the site directed mutagenesis protocols described herein and known within the art, a skilled investigator may induce individual nucleotide changes which result in an altered amino acid sequence or which preserve an amino acid sequence but introduce a desired restriction enzyme recognition sequence into the gene. This new restriction endonuclease recognition site may then be used to cut the gene at that particular point and use it to a gene or segment of another accessory molecule ligand gene. In addition to these methods, one of ordinary skill in the art will understand that an entire chimeric accessory molecule ligand gene may be synthesized using synthetic methods known in the art. This methodology only requires that the skilled artesian

generating nucleotide sequence of a chimeric accessory molecule ligand gene and provide that sequence to a company which is capable of synthesizing such a gene.

5 B. Genetic Constructs

 The present invention contemplates the use of accessory molecule ligand genes or chimeric accessory molecule ligand genes which are present in various types
10 of genetic vectors. A genetic vector refers to a DNA molecule capable of autonomous replication in a cell into which another DNA segment can be inserted to cause the additional DNA segments to replicate. Vectors capable of expressing genes contained in that vector are
15 referred to as "expression vectors." Thus, the genetic vectors and expression vectors of the present invention are recombinant DNA molecules which comprise at least two nucleotide sequences not normally found together in nature.

20 The genetic vectors useful in the present invention contain an accessory molecule ligand gene which encodes an accessory molecule ligand which is optionally operatively linked to a suitable transcriptional or translational regulatory nucleotide sequence, such as
25 one derived from a mammalian, microbial, viral, or insect gene. Such regulatory sequences include sequences having a regulatory role in gene expression, such as a transcriptional promoter or enhancer, an operator sequence to control transcription, a sequence
30 encoding a ribosomal binding site within the messenger RNA and appropriate sequences which control transcription, translation initiation or transcription termination.

 Particularly useful regulatory sequences include
35 the promoter regions from various mammalian, viral,

microbial, and insect genes. The promoter region directs an initiation of transcription of the gene and causes transcription of DNA through and including the accessory molecule ligand gene. Useful promoter regions include the promoter found in the Rous Sarcoma Virus (RSV) - long terminal repeat (LTR), human cytomegalovirus (HCMV) enhancer/promoter region lac promoters, and promoters isolated from adenovirus, and any other promoter known by one of ordinary skill in the art would understand to be useful for gene expression in eukaryotes, prokaryotes, viruses, or microbial cells. Other promoters that are particularly useful for expressing genes and proteins within eukaryotic cells include mammalian cell promoter sequences and enhancer sequences such as those derived from polyoma virus, adenovirus, simian virus 40 (SV40), and the human cytomegalovirus. Particularly useful are the viral early and late promoters which are typically found adjacent to the viral origin of replication in viruses such as the SV40. Examples of various promoters which have been used in expression vectors have been described by Okama and Berg (Mol. Cell. Biol. 3:280, 1983), the pMLSVN SV40 described by Kossman et al., Nature 312:768 (1984). One of ordinary skill in the art will understand that the selection of a particular useful promoter depends on the exact cell lines and the other various parameters of the genetic construct to be used to express the accessory molecule ligand gene or the chimeric accessory molecule ligand gene within a particular cell line. In addition, one of ordinary skill in the art will select a promoter which is known to express genes in the target cell at a sufficiently high level to be useful in the present invention.

The genetic vectors and expression vectors of the present invention optionally contain various additional

regulatory sequences including ribosome binding sites which allow the efficient translation of the messenger RNA produced from an expression vector into proteins, the DNA sequence encoding various signals peptides which
5 may be operatively linked to the accessory molecule ligand gene or the chimeric accessory molecule ligand gene. The signal peptide, if present, is expressed as a precursor amino acid which enables improved extracellular secretion of translation fusion
10 polypeptide.

The genetic constructs contemplated by the present invention therefore include various forms of accessory molecule ligand genes described above which are operatively linked to either a promoter sequence or a
15 promoter and enhancer sequence and also operatively linked to a polyadenylation sequence which directs the termination and polyadenylation of messenger RNA. It is also contemplated that the genetic constructs of the present invention will contain other genetic sequences
20 which allow for the efficient replication and expression of that construct within the desired cells. Such sequence may include introns which are derived from native accessory molecule ligand genes or, for example, from a virus gene.

25 The present invention also contemplates gene therapy vectors which are able to directly infect mammalian cells so as to introduce the desired accessory molecule ligand gene or chimeric accessory molecule ligand gene into that cell. These gene therapy vectors
30 are useful for directly infecting cells which have been isolated from an animal or patient, or can be directly introduced into an animal or patient and thereby directly infect the desired cell within that animal or patient.

Many types of gene therapy vectors which are able to successfully transfer genes and cause the expression of desired foreign DNA sequences have been developed and described in the literature. For example, the article
5 entitled "Gene Transfer Vectors for Mammalian Cells" in Current Comm. Mol. Biol., Cold Springs Harbor Laboratory, New York (1987). Further, naked DNA can be physically introduced into eukaryotic cells including human cells by transvection using any number of
10 techniques including calcium phosphate transfection (Berman et al., Proc. Natl. Acad. Sci. USA, 81:7176 (1984)), DEAE-Dextran Transfection, protoplast fusion (Deans et al., Proc. Natl. Acad. Sci. USA, 81:1292 (1984)), electroporation, liposome fusion, polybrene
15 transfection and direct gene transfer by laser micropuncture of the cell membrane. In addition, one of ordinary skill in the art will understand that any technique which is able to successfully introduce the DNA into a cell in such a manner as to allow it to
20 integrate into the genome of a cell and allow the expression of the desired gene would be useful in the present invention.

Specifically, gene therapy vectors which utilize recombinant infectious virus particles for gene delivery
25 have been widely described. See, for example, Brody, S. L. and R. G. Crystal, Ann. N. Y. Acad. Sci., 716:90 (1994); Srivastava, A., Blood. Cells, 20:531 (1994); Jolly, D., Cancer Gene Ther., 1:51 (1994); Russell, S. J., Eur. J. Cancer, 30A:1165 (1994); Yee, J. K., T. Friedmann, and J. C. Burns, Methods Cell Biol., 43 Pt
30 A:99 (1994); Boris-Lawrie, K. A. and H. M. Temin, Curr. Opin. Genet. Dev., 3:102 (1993); Tolstoshev, P., Annu. Rev. Pharmacol. Toxicol., 33:573 (1993); and, Carter, B. J., Curr. Opin. Biotechnol., 3:533 (1992). The present
35 invention contemplates the use of gene therapy vectors

to carry out the desired methodology of the present invention by introducing a gene encoding an accessory molecule ligand gene or a chimeric accessory molecule ligand gene into the cell. Many viral vectors have been
5 defined and used as gene therapy vectors and include virus vectors derived from simian virus 40 (SV40), adenoviruses, adeno-associated viruses, and retroviruses. One of ordinary skill in the art will understand that useful gene therapy vectors are vectors
10 which are able to directly introduce into the target cells the DNA which encodes the accessory molecule ligand and allow that DNA to persist in the cell so as to express the accessory molecule ligand in the desired manner within the cell.

15 The gene therapy vectors of the present invention are useful for introducing accessory molecule ligand genes into a variety of mammalian cells including human cells. The particular cells infected by the gene therapy vector will depend on the various specifics of
20 the vector and such vectors can be used to introduce the accessory molecule ligand genes of the present invention into hematopoietic or lymphoid stem cells, antigen presenting cells, embryonic stem cells, and other cells which are capable of presenting antigen within the
25 immune system including cells which have CD40 on their surface. Further, such gene therapy vectors are able to introduce a gene encoding an accessory molecule ligand gene into a human neoplastic cell such as a lymphoma, leukemia, AML, CLL, CML, AMML, CMML, breast cancer, lung
30 cancer, ovarian cancer or any tumor capable of acting as antigen presenting cells or cells which can stimulate bystander antigen presenting cells. Further, the contemplated gene therapy vectors may be used to introduce the accessory molecule ligand genes of the
35 present invention into cells which have been engineered

to make those cells capable of presenting antigen to the immune system.

5 III. Cells Containing Genetic Constructs Encoding an
Accessory Molecule Ligand or Chimeric Accessory
Molecule Ligand

10 The present invention also contemplates various cells which contain the genetic constructs of the present invention. These cells contain the constructs which encode the accessory molecule ligand gene and thus contain the various genetic elements described in Section II.B. above. These cells may be microbial cells, eukaryotic cells, insect cells, and various
15 mammalian cells including human cells. In preferred embodiments of the present invention, these cells include various neoplastic cells including human neoplastic cells. These neoplastic cells may be of any cell type and include cells of the immune system, and
20 other blood cells. Particularly preferred are any neoplastic cells which may function as an antigen presenting cells within the immune system or which may stimulate bystander antigen presenting cells by expression of a transgenic accessory cell molecule of
25 the present invention. Typically these neoplastic which are able to function to present antigen to the immune system have or have had an accessory molecule, such as the CD40 molecule, on the cell surface. Generally, these cells are naturally capable of presenting antigen
30 to the immune system, but the present invention also contemplates the introduction of accessory molecule ligand genes into a cell which is not naturally able to present antigen to the immune system but which has been genetically engineered to make that cell capable of
35 presenting antigen to the immune system. Typically, these cells include various known cell types such as

monocytes, macrophages, B cells, Langerhans cells, interdigitating cells, follicular dendritic cells or Kupffer cells and the like which have become neoplastic. In addition, the present invention also contemplates
5 cells from various carcinomas, breast, ovarian and lung cancers which contain the genetic constructs described herein. In other preferred embodiments, an accessory molecule ligand gene of the present invention is placed into cells which may be injected into a treatment site
10 such as a tumor bed or joint. For example, the accessory molecule ligand gene of the present invention may be inserted into a fibroblast cell and the accessory molecule ligand expressed on the surface of that cell. The fibroblasts are then injected into the treatment
15 site and cause the desired immuno effect due to the presence of the accessory molecule ligand on the surface of those cells. These cells stimulate other immune cells present in that treatment site (bystander cells). This process then results in the desired effect on the
20 immune system.

IV. Methods Utilizing Genetic Vectors and Constructs Containing an Accessory Molecule Ligand Gene

25 The present invention contemplates methods of altering the immunoreactivity of human cells using a method which includes introducing a gene encoding an accessory molecule ligand gene into the human cells so that the accessory molecule ligand encoded by that gene
30 is expressed on the surface of those cells. The present invention is useful for any human cells which participate in an immune reaction either as a target for the immune system or as part of the immune system which responds to the foreign target. A large variety of
35 methods are contemplated in which the final result is that the accessory molecule ligand gene is introduced

into the desired cells. These methods include ex vivo methods, in vivo methods and various other methods which involve injection of DNA, genetic vectors or gene therapy vectors into the animal or human, including
5 injection directly into the tumor bed present in any animal or human.

Ex vivo methods are contemplated wherein the cells into which the accessory molecule ligand gene is to be introduced are isolated from the animal or patient and
10 then the gene is introduced into those isolated cells using suitable methods. Examples of useful ex vivo methods have been described for example by Raper, S. E., M. Grossman, D. J. Rader, J. G. Thoene, B. J. Clark, D. M. Kolansky, D. W. Muller, and J. M. Wilson, Ann. Surg.,
15 223:116 (1996); Lu, L., R. N. Shen, and H. E. Broxmeyer, Crit. Rev. Oncol. Hematol., 22:61 (1996); Koc, O. N., J. A. Allay, K. Lee, B. M. Davis, J. S. Reese, and S. L. Gerson, Semin. Oncol., 23:46 (1996); Fisher, L. J. and J. Ray, Curr. Opin. Neurobiol., 4:735 (1994); and,
20 Goldspiel, B. R., L. Green, and K. A. Calis, Clin. Pharm., 12:488 (1993). D. Dilloo et al., in Blood 90:1927-1933 (1997), describe a method, using CD40L-activated cells, for treating B-acute lymphoblastic leukemia (ALL). They cocultured leukemia cells with
25 fibroblasts infected with a retroviral vector encoding CD40L, then injected the cell mix into mice. Such an approach, if taken in humans, would differ from that contemplated here in that the therapeutic cells are stimulated in vitro, by another cell line expressing the
30 accessory molecule ligand. Schultze, J.L. et al., in Blood 89: 3806-3816 (1997), describe a method for stimulating T-TILs (tumor-infiltrating T cells) cytotoxic for follicular lymphoma (FL) cells by exposing them, in vitro, to FL B cells which were previously
35 cultured with CD40L-expressing fibroblasts. They

propose an adoptive immunotherapy in which T-TILS stimulated in this manner are transfused into patients. This method also requires in vitro stimulation, of the cells to be transfused, with another cell line
5 expressing an accessory molecule.

Following the introduction of the gene, including any optional steps to assure that the accessory molecule ligand gene has been successfully introduced into those isolated cells, the isolated cells are introduced into
10 the patient either at a specific site or directly into the circulation of the patient. In preferred embodiments of the present invention, cell surface markers, including molecules such tumor markers or antigens identify the cells are used to specifically
15 isolate these molecules from the patient. One of ordinary skill in the art will understand that such isolation methods are well known and include such methodologies as fluorescence activated cell sorting (FACS), immunoselection involving a variety of formats
20 including panning, columns and other similar methods.

The present invention also contemplates introducing the accessory molecule ligand gene into the desired cells within the body of an animal or human patient without first removing those cells from the patient.
25 Methods for introducing genes into specific cells in vivo, or within the patient's body are well known and include use of gene therapy vectors and direct injection of various genetic constructs into the animal or patient. Examples of useful methods have been described
30 by Danko, I. and J. A. Wolff, Vaccine, 12:1499 (1994); Raz, E., A. Watanabe, S. M. Baird, R. A. Eisenberg, T. B. Parr, M. Lotz, T. J. Kipps, and D. A. Carson, Proc. Natl. Acad. Sci. U. S. A., 90:4523 (1993); Davis, H. L., R. G. Whalen, and B. A. Demeneix, Hum. Gene Ther., 4:151
35 (1993); Sugaya, S., K. Fujita, A. Kikuchi, H. Ueda, K.

Takakuwa, S. Kodama, and K. Tanaka, Hum. Gene Ther., 7:223 (1996); Prentice, H., R. A. Kloner, Y. Li, L. Newman, and L. Kedes, J. Mol. Cell Cardiol., 28:133 (1996); Soubrane, C., R. Mouawad, O. Rixe, V. Calvez, A. Ghoumari, O. Verola, M. Weil, and D. Khayat, Eur. J. Cancer, 32A:691 (1996); Kass-Eisler, A., K. Li, and L. A. Leinwand, Ann. N. Y. Acad. Sci., 772:232 (1995); DeMatteo, R. P., S. E. Raper, M. Ahn, K. J. Fisher, C. Burke, A. Radu, G. Widera, B. R. Claytor, C. F. Barker, and J. F. Markmann, Ann. Surg., 222:229 (1995); Addison, C. L., T. Braciak, R. Ralston, W. J. Muller, J. Gauldie, and F. L. Graham, Proc. Natl. Acad. Sci. U. S. A., 92:8522 (1995); Hengge, U. R., P. S. Walker, and J. C. Vogel, J. Clin. Invest., 97:2911 (1996); Felgner, P. L., Y. J. Tsai, L. Sukhu, C. J. Wheeler, M. Manthorpe, J. Marshall, and S. H. Cheng, Ann. N. Y. Acad. Sci., 772:126 (1995); and, Furth, P. A., A. Shamay, and L. Hennighausen, Hybridoma, 14:149 (1995). In a typical application, a gene therapy vector containing an accessory molecule ligand gene is introduced into the circulation or at a localized site of the patient to allow the gene therapy vector to specifically infect the desired cells. In other preferred embodiments the gene therapy vector is injected directly into the tumor bed present in an animal which contains at least some of the cells into which the accessory molecule ligand gene is to be introduced.

The present invention also contemplates the direct injection of DNA from a genetic construct which has a promoter and accessory molecule ligand gene followed by a polyadenylation sequence into a patient or animal. Examples of such useful methods have been described by Vile, R. G. and I. R. Hart, Ann. Oncol., 5 Suppl 4:59 (1994). The genetic construct DNA is directly injected into the muscle or other sites of the animal or patient

or directly into the tumor bed of the animal or patient. Alternatively, DNA from a genetic construct containing at least an accessory molecule ligand gene is used and directly injected into the animal.

5 In preferred embodiments of the present invention, the immune reaction or response of a human patient or animal is altered by introducing the accessory molecule ligand gene into cells, including human cells which have an accessory molecule present on the cell surface. Such
10 cells include human cells, human antigen presenting cells and optionally these cells may be neoplastic antigen presenting cells which have the capacity to express the accessory molecule on the surface of the cell or cells which are capable of stimulating. In some
15 embodiments, the amount of accessory molecule present on the surface of the cells into which the accessory molecule ligand gene is to be introduced is very small and such small amounts of the accessory molecule may result from down-regulation of that accessory molecule
20 on the surface of such cells. In some embodiments, the cells into which the accessory molecule ligand gene is introduced have at least low levels of the CD40 molecule present on the cell surface or are derived from cells which did express the CD40 ligand molecule on the cell
25 surface but have reduced or eliminated that expression.

The preferred methods of altering the immunoreactivity of a particular cell are applicable to mammalian cells including human cells. These human
30 cells may include neoplastic human cells such as human lymphomas, leukemias, and other malignancies including breast, lung and ovarian cancers. In some preferred embodiments the cells are normal antigen presenting cells of a human patient such as monocytes, macrophages, B cells, Langerhans cells, interdigitating cells,
35 follicular dendritic cells, Kupffer cells, and other

similar cells. In preferred embodiments, the cells are lymphocytes which acquire altered immunoreactivity when the accessory molecules of the present invention are introduced into those cells. In other preferred

5 embodiments, the cells may be neoplastic or normal cells which are capable of stimulating bystander antigen presenting cells when the accessory molecule ligand genes of the present invention are introduced into these cells. The present invention also contemplates that

10 cells which are not naturally capable of presenting antigen to the immune system may be genetically engineered to introduce the genes encoding the molecules required for antigen presentation, including genes encoding an accessory molecule, and thus allow these

15 cells to act as artificial antigen presenting cells. The accessory molecule ligand gene may then be introduced into these artificial antigen presenting cells. Various tests are well known in the literature to determine whether a particular cell is able to

20 function as an antigen presenting cell, such as cell proliferation or the production of lymphokines and therefore this aspect of the present invention may be easily determined.

In addition to the above normal human cells, the

25 present invention also contemplates introducing the accessory molecule ligand gene into various neoplastic or malignant cells which optionally are antigen presenting cells. Such human neoplastic cells which are contemplated include leukemias, lymphomas, AML, AMML, or

30 CMML, CML, CLL and any neoplastic cell which is capable of stimulating bystander antigen presenting cells when an accessory molecule ligand is introduced into that cell. Also contemplated are neoplastic cells such as a breast, ovarian or lung cancer cell which is capable of

35 or is engineered to act as an antigen presenting cell.

However, the present immunomodulation also applicable to other malignancies not specifically identified and thus would include any tumor of any cell capable of presenting antigen within the animal or human immune system or any cell which is capable of acting as an antigen presenting cell or capable of stimulating bystander antigen presenting cells after an accessory molecule ligand gene has been introduced into those cells. Generally these antigen presenting cells have accessory molecules on the surface of the cells.

The present methods of altering the immunoreactivity of a human or animal cell contemplate the introduction of an accessory molecule ligand gene into the cells for which altered immunoreactivity is desired. The genes useful in the present invention include the wide range of accessory molecule ligand genes and chimeric accessory molecule ligand genes identified above and in preferred embodiments include at least a portion of the murine CD40 ligand gene. In particularly preferred embodiments, the accessory molecule ligand gene introduced into the cells using the methods of the present invention is selected to correspond to the accessory molecule present on the surface of the cells for which altered immunoreactivity is desired. In one particular application of the present invention, the immunoreactivity of a cell which expresses the CD40 molecule on the cell surface would be accomplished by introducing the gene which encodes the CD40 ligand molecule and more preferably the murine CD40 ligand molecule.

The present invention also contemplates altering the immunoreactivity of human or animal cells by introducing an accessory molecule ligand gene which is a chimeric accessory molecule ligand gene into the cell. The various useful chimeric accessory molecule ligand

genes were identified above and could include a wide variety of molecules and allow the unique properties of those chimeric accessory molecule ligand genes to be utilized to alter the immunoreactivity of the target
5 cells. In preferred embodiments, useful chimeric accessory molecule ligand genes are genes which encode at least a portion of the accessory molecule ligand which is capable of binding the accessory molecule present on the surface of the cells for which altered
10 immunoreactivity is desired.

The methods of the present invention for altering the immunoreactivity contemplate the use of genetic vectors and genetic constructs including gene therapy vectors which encode an accessory molecule ligand and
15 therefore contain an accessory molecule ligand gene. Typically, the genetic vectors and genetic constructs including the gene therapy vectors of the present invention have a promoter which is operatively linked to the accessory molecule ligand gene followed by a
20 polyadenylation sequence. In other embodiments, the only requirement is that the genetic vectors, genetic constructs, and gene therapy vectors of the present invention contain the accessory molecule ligand gene or the chimeric accessory molecule ligand gene.

25

V. Methods of Treating Neoplasia

The present invention also contemplates methods of treating human neoplasia comprising inserting into a
30 human neoplastic cell a gene which encodes an accessory molecule ligand so that the accessory molecule ligand is expressed on the surface of the neoplastic cells. The present invention contemplates treating human neoplasia both in vivo, ex vivo and by directly injecting various
35 DNA molecules containing a gene which encodes an

accessory molecule ligand into the patient. However, at a minimum, the present methods for treating human neoplasia involve inserting the gene encoding the accessory molecule ligand into the neoplastic cells in such a way as to allow those neoplastic cells to express the accessory molecule ligand on the cell surface. The expression of the accessory molecule ligand gene in these neoplastic cells modulates the immune system to cause the neoplasia to be reduced or eliminated.

In a preferred method of treating human neoplasia, the method further comprises the steps of first obtaining the human neoplastic cells from a human patient and then inserting into the isolated human neoplastic cells a gene which encodes an accessory molecule ligand so that the accessory molecule ligand is expressed on the surface of the neoplastic cells. The human neoplastic cells having the accessory molecule ligand on the surface of that cell are then infused back into the human patient. One of ordinary skill in the art will understand that numerous methods are applicable for infusing the altered human neoplastic cells containing the gene encoding the accessory molecule ligand back into the patient and that these methods are well known in the art.

The contemplated methods of treating human neoplasia are applicable to a wide variety of human neoplasias including lymphomas, leukemias, and other malignancies. In preferred embodiments the human neoplasia is a neoplasia which involves the antigen presenting cells of the human immune system and includes monocytes, macrophages, B cells, Langerhans cells, interdigitating cells, follicular dendritic cells, Kupffer cells, and the like. In other preferred embodiments, the human neoplasia is a leukemia, a lymphoma, AML, AMML, CMML, CML or CLL, lung cancer,

breast cancer, ovarian cancer and other similar neoplasias.

5 The genetic vectors, genetic constructs and gene therapy vectors useful in the methods of treating human neoplasia of the present invention have been disclosed above and include constructs in which a promoter is operatively linked to the accessory molecule ligand gene or the chimeric accessory molecule ligand gene which is in turn operatively linked to a polyadenylation
10 sequence. The methods of treating human neoplasia contemplate the use of genetic constructs, genetic vectors and gene therapy vectors as described in this specification. In addition, the present invention contemplates the use of DNA which contains at least a
15 gene encoding an accessory molecule ligand gene. This gene may or may not contain a promoter and other regulatory sequences.

In preferred embodiments of the present invention, the cells comprising the human neoplasia are located in
20 at least one defined site termed a tumor bed within the human patient. This tumor bed typically contains the tumor or neoplastic cell together with a number of other cells which are associated with the tumor or neoplastic cells. The present invention contemplates methods of
25 treating such human neoplasia present in a tumor bed by injecting into the tumor bed of the patient, a gene which encodes an accessory molecule ligand so that the accessory molecule ligand is expressed on the surface of the tumor cells thereby causing the cells to participate
30 in an immune reaction. The gene which encodes the accessory molecule ligand may be present as part of a gene therapy vector, genetic construct or genetic vector.

In preferred embodiments, the accessory molecule
35 ligand gene is a chimeric accessory molecule ligand gene

which has at least a portion of the murine CD40 ligand gene is used. In other preferred embodiments, the accessory molecule ligand encoded is capable of binding an accessory molecule present on the human neoplasia to be treated.

The various gene therapy vectors used in the treatment methods of the present invention include vectors which are capable of directly infecting human cells. Such vectors have been described in the literature and are readily adaptable to the methods described in the present invention.

The present invention contemplates the use of any type of gene therapy including the methods of Raper, S.E. et al., Ann. Surg., 223:116 (1996); Lu, L. et al., Crit. Rev. Oncol. Hematol., 22:61 (1996); Koc, O. N. et al., Semin. Oncol., 23:46 (1996); Fisher, L. J. et al., Curr. Opin. Neurobiol., 4:735 (1994); Goldspiel, B. R. et al., Clin. Pharm., 12:488 (1993); Danko, I. et al., Vaccine, 12:1499 (1994); Raz, E. et al., Proc. Natl. Acad. Sci. U.S.A., 90:4523 (1993); Davis, H. L. et al., Hum. Gene Ther., 4:151 (1993); Sugaya, S. et al., Hum. Gene Ther., 7:223 (1996); Prentice, H. et al., J. Mol. Cell Cardiol., 28:133 (1996); Soubrane, C. et al., Eur. J. Cancer, 32A:691 (1996); Kass-Eisler, A. et al., ann. N. Y. Acad. Sci., 772:232 (1995); DeMatteo, R. P. et al., Ann. Surg., 222:229 (1995); Addison, C. L. et al., Proc. Natl. Acad. Sci. U.S.A., 92:8522 (1995); Hengge, U. R. et al., J. Clin. Invest., 97:2911 (1996); Felgner, P. L. et al., Ann. N. Y. Acad. Sci., 772:126 (1995); Furth, P.A., Hybridoma, 14:149 (1995); Yovandich, J. et al., Hum. Gene Ther., 6:603 (1995); Evans, C.H. et al., Hum. Gene Ther., 7:1261.

VI. Methods of Vaccination

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The present invention contemplates methods of vaccinating an animal against a predetermined organism comprising administering to that animal a vaccine containing immunogenic animal antigens capable of causing an immune response in that animal against the desired organism together with a vector containing a gene encoding an accessory molecule ligand. The present invention also contemplates methods of vaccinating an animal which include administering the genes which encode the immunogenic antigen capable of causing a desired immune response or altering the immune response to a particular antigen together with a vector containing a gene including the accessory molecule ligand gene. In this particular embodiment, the vector or vectors introduced encode the immunogenic antigens desired and the desired accessory molecule ligand. The present invention also contemplates that the gene or genes encoding the immunogenic peptide or peptides may be present on the same vector as is the gene or genes encoding the accessory molecule ligand.

The vaccination methods of the present invention are general in that they may be used to produce a vaccination against any predetermined organism, such as a virus, a bacteria, a fungus or other organism. In addition, the present vaccination methods may be used to produce an immune response against a neoplastic cell.

In other preferred embodiments, the vaccination methods of the present invention utilize a genetic vector, a genetic construct or a gene therapy vector which contains an accessory molecule ligand gene which is a chimeric accessory molecule ligand gene. That chimeric accessory molecule ligand gene preferably contains at least a portion of the murine CD40 ligand gene. In other preferred embodiments, the vaccination method utilizes a DNA molecule which encodes at the

minimum the accessory molecule ligand gene or a chimeric accessory molecule ligand gene. This particular DNA may or may not include a promoter sequence which directs the expression of the accessory molecule ligand gene.

5 The present invention also contemplates that the vaccination method may utilize a genetic vector which is capable of expressing an accessory molecule ligand within a particular cell or organism together with a vector which is capable of expressing at least a single
10 polypeptide from an andovirus. This andovirus polypeptide may be expressed from the same or different vector which expresses the accessory molecule ligand in that cell. In this particular embodiment, the andovirus polypeptide is also expressed in at least one cell type
15 within the organism and serves to modulate the immune response found in response to this vaccination protocol.

 The present invention also contemplates the introduction of an accessory molecule ligand gene into cells which are present in the joints of patients with
20 rheumatoid arthritis. In preferred embodiments, the accessory molecule ligand gene introduced comprises at least a portion of the Fas ligand gene and upon expression the accessory ligand induces the cell death of cells expressing Fas on the cell surface. This
25 process leads to the reduction of the destructive inflammatory process.

 The following examples are provided to illustrate various aspects of the present invention and do not limit the scope of that invention.

30

VII. Methods of Treating Arthritis

 The present invention also contemplates methods of treating arthritis comprising inserting into a joint,
35 cells which have been transformed with an accessory

molecule, such as the Fas ligand. In preferred
embodiments, the expression of that accessory molecule
ligand or the stability of that molecule on the surface
of the cells has been altered. In these preferred
5 embodiments, the accessory molecule ligand functions in
an enhanced manner to aid in the treatment of arthritis
within the joint. The present invention contemplates
treating human arthritis both in vivo, ex vivo, and by
directly injecting various DNA molecules containing
10 genes which encode the useful accessory molecule ligand
into the patients. Various useful protocols may be
designed to rheumatoid arthritis including those
described in the example section below.

The present invention contemplates the treatment of
15 arthritis utilizing accessory molecule ligand genes
which may be chimeric accessory molecule ligand genes
comprised of portions of that gene being derived from
two different accessory molecule ligand genes. In other
embodiments, the chimeric accessory molecule ligands may
20 be produced by utilizing domains from the same accessory
molecule ligand gene. The resulting chimeric accessory
molecule ligands have an altered stability on the
surface of cells upon which they are expressed. This
altered stability modulates the function of the immune
25 system in the local environment around the cells in
which these chimeric accessory molecule ligands are
expressed. For example, in certain preferred
embodiments, Fas ligand stability is altered on the
surface of cells within a joint of a patient suffering
30 from arthritis. This altered stability modulates the
immune system and causes the cells to be targeted for
apoptosis and thus reducing the immune response within
the inflamed joint. In other embodiments, the accessory
molecule ligand genes described within are altered such
35 that the resulting accessory molecule ligand has an

altered stability and causes an immunomodulatory effect which can be useful in the treatment of arthritis.

The present invention contemplates in preferred embodiments that chimeric accessory molecule ligands
5 genes be utilized in the treatment of arthritis. These chimeric accessory molecule ligand genes preferably contain at least a portion of the Fas ligand gene Domain IV, which carries the effect or function for Fas ligand. In preferred embodiments, at least in the portion of
10 that domain, is present which allows Fas ligand to have its biologic effects. In other preferred chimeric accessory molecule ligands, those ligands contain domains from other accessory molecule ligand genes of the present invention or from a different domain of the
15 same accessory molecule ligand. Particularly preferred are Fas chimeric accessory molecule ligand genes made up on Domain IV of the human Fas ligand operatively linked with Domain III of the mouse Fas ligand. This particular combination results in more stable Fas ligand
20 and thus, by replacing Domain III of human Fas ligand with Domain III of the mouse ligand, the activity of the human Fas ligand gene is altered.

Alternatively, in other preferred embodiments, the murine Fas ligand gene is used to encode the murine Fas
25 ligand on the surface of cells in place of the human Fas ligand. The murine Fas ligand is more stable than the human Fas ligand and thus, alters the Fas ligand activity in the joint. The resulting alter Fas ligand activity is useful in the treatment of rheumatoid
30 arthritis.

Further preferred embodiments include embodiments in which the effect or function present on Domain IV of the human Fas ligand is combined with other domains from other accessory molecule ligands. For example,
35 CD70 Domain III is more stable than Domain III of the

human Fas ligand and thus the chimeric accessory molecule ligand made up of Domain III from the human CD70 and Domain IV of the Fas ligand together with other supporting domains would be more stable. The increased
5 stability leads to increase Fas ligand activity. In other preferred embodiments, Domain III of the Fas ligand is replaced with multiple copies of a domain or domains. Such multiple copies of domains include domains made up of two or more copies of other domains
10 such as Domains III or I of the CD70 molecule.

In other preferred embodiments, the present invention contemplates accessory molecule ligand genes, such as Fas ligand genes, in which a cleavage site for matrix-metalloproteinase (MMP), have been removed from
15 the accessory molecule ligand. MMP cleavage and recognition sites, charted in Figure 28, are discussed in Smith, M.M. et al., Journal of Biol. Chem. 270:6440-6449 (95) and Nagase, H., and G.B. Fields, Biopolymers (Peptide Science) 40:399-416 (96). In preferred
20 embodiments, at least one MMP site has been removed from at least Domain III of the Fas ligand gene. The removal of the MMP site from the Fas ligand gene makes the Fas ligand more stable and thus, more effective in the treatment of arthritis.

25 In other preferred embodiments, chimeric accessory molecule ligand genes are comprised of portions of the human Fas ligand gene with other domains from other human accessory molecule ligands or domains from accessory molecules derived from other species. For
30 example, the present invention contemplates the use of domains from CD40 ligand, CD70 ligand, CD30 ligand, TNF-related apoptosis inducing ligand (TRAIL), TNF- α as well as mutants of human Fas ligand and murine Fas ligand. Production of such chimeric accessory molecule ligands
35 is easily accomplished by manipulating and producing

accessory molecule ligand genes which are chimeric and thus has portions derived from at least two different accessory molecule ligand genes.

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EXAMPLES

1. Expression of Human and Mouse Accessory
Molecule Ligand in Human CLL Cells

5

a. Construction of a Genetic Construct and Gene
Therapy Vector Containing a Human and Mouse
Accessory Molecule Ligand Gene

10 Either the human accessory molecule ligand gene
(human CD40 ligand) or the murine accessory molecule
ligand gene (murine CD40 ligand) was constructed
utilizing the respective human and murine genes. Each
of these genes was cloned in the following manner.

15

i. Murine CD40-L cloning

Total RNA was isolated using the RNA STAT-60 kit
(Tel-Test "B" Inc., Friendswood, TX) from 1×10^7 B6
20 mouse splenocytes that were previously activated for 8
hours with immobilized CD3-specific mAb. cDNA was then
synthesized with the Superscript cDNA synthesis kit
(Gibco BRL, Grand Island, NY) using oligo-dT primers.
The murine CD40 ligand (mCD40-L) gene was then amplified
25 from the cDNA by PCR using the following mCD40-L
specific primers. 5'-GTAAAGCTTTTCAGTCAGCATGATAGAA (SEQ
ID NO: 26), 5'-GTTTCTAGATCAGAGTTTGAGTAAGCC (SEQ ID NO:
27). The amplified mCD40-L PCR product was subcloned
into the HindIII and XbaI sites of the eukaryotic
30 expression vector pcDNA3 (Invitrogen, San Diego, CA). A
DNA fragment encompassing the CMV promoter, mCD40-L
gene, and polyadenylation signal was released from this
plasmid construct after restriction digestion with BglII
and XhoI enzymes. This DNA fragment was then subcloned
35 into the shuttle plasmid MCS(SK)pXCX2 (Spessot R, 1989,

Virology 168:378) that was designated mCD40-L pXCX2. This plasmid was used for adenovirus production as described below.

5 ii. Human CD40-L Cloning

A plasmid containing the gene for human CD40-L was used to produce the human CD40-L gene used herein. The sequence of this gene is available and thus this source
10 of the gene was used merely for convenience. See GenBank accession no. X67878. This plasmid was used for PCR amplification of the human CD40-L gene using the specific primers, sense primer 5' CCAAGACTAGTTAACACAGCATGATCGAAA 3' (SEQ ID NO: 28) and
15 antisense primer 5' CCAATGCGGCCGCACTCAGAATTCAACCTG 3' (SEQ ID NO: 29).

These primers contain flanking restriction enzyme sites for subcloning into the eukaryotic expression plasmid pRc/CMV (Invitrogen). The PCR amplified CD40-L
20 fragment was subcloned into the SpeI and NotI sites of pRc/CMV and designated hCD40-L pRc/CMV. A BglII and XhoI fragment encompassing the CMV promoter, hCD40-L gene, and polyadenylation signal was then released from this plasmid and subcloned into the shuttle plasmid
25 MCS(SK)pXCX2 as described above. This plasmid was designated hCD40-L pXCX2. This plasmid was used for adenovirus production as described below.

30 iii. Adenovirus Synthesis

Either mCD40-L pXCX2 or hCD40-L pXCX2 plasmids were co-transfected with pJM17 (Graham and Prevec, 1991, Methods in Molecular Biology, Vol 7) into 293 cells (American Type Culture Collection, Rockville, MD) using
35 the calcium phosphate method (Sambrook, Fritsch, and

Maniatis, 1989, Molecular Cloning, A Laboratory Manual,
2nd edition, chapter 16:33-34). Isolated adenovirus
plaques were picked and expanded by again infecting 293
cells. High titer adenovirus preparations were obtained
5 as described (Graham and Prevec, 1991, Methods in
Molecular Biology, Vol 7), except for the following
modifications. The cesium chloride gradient used for
concentrating viral particles was a step gradient, with
densities of 1.45 g/cm³ and 1.2 g/cm³. The samples were
10 spun in a SW41 rotor (Beckman, Brea, CA) at 25,000 rpm
at 4°C. The viral band was desalted using a Sephadex
G25 DNA grade column (Pharmacia, Piscataway, NJ). The
isolated virus was stored at 70°C in phosphate buffered
saline with 10% glycerol. The virus titer was
15 determined by infecting 293 cells with serial dilutions
of the purified adenovirus and counting the number of
plaques formed. Viral titers typically ranged from 10¹⁰
to 10¹² plaque forming units/ml (PFU/ml).

20 b. Introduction of a Murine and Human Accessory
Molecule Ligand Gene into CLL Cells and HeLa
Cells

For adenovirus infection, 10⁶ freshly thawed and
25 washed CLL cells or HeLa cells were suspended in 0.5 to
1 mL of culture medium for culture at 37°C in a 5% CO₂-
in-air incubator. Adenovirus was added to the cells at
varying multiplicity of infection (MOI), and the
infected cells were cultured for 48 hours, unless
30 otherwise stated, before being analyzed for transgene
expression.

c. Expression of an Accessory Molecule Ligand
Gene in CLL Cells and HeLa Cells

5 The CLL and HeLa cells which were infected with the
adenovirus vector containing either mouse or human CD40
ligand genes prepared in Example 1b. were then stained
with commercially available monoclonal antibodies
immunospecific for either human or mouse CD40 ligand
(Pharmingen, San Diego, CA) using the manufacturer's
10 directions. The CLL and HeLa cells were washed in
staining media (SM) consisting of RPMI-1640, 3% fetal
calf serum and 0.05% sodium azide and containing
propidium iodide and then analyzed on a FACScan (Becton
Dickinson, San Jose, CA). Dead cells and debris were
15 excluded from analysis by characteristic forward and
side light scatter profiles and propidium iodide
staining. Surface antigen expression was measured as
the mean fluorescence intensity ratio (MFIR). MFIR
equals the mean fluorescence intensity (MFI) of cells
20 stained with a specific FITC-conjugated MoAb, divided by
the MFI of cells stained with a control IgG-FITC. This
method controls for the nonspecific increases in auto-
fluorescence seen in larger, more activated cells.

The histograms, generated for the CLL cells and
25 HeLa cells containing either a genetic vector containing
the human CD40 ligand gene or the murine CD40 ligand
gene and the appropriate controls, are shown in Figure
3A-3D. The expression of both the murine and human
accessory molecule ligand gene (CD40 ligand) in HeLa
30 cells is shown in Figures 3A and 3B, respectively. The
expression of the murine and human accessory molecule
ligand in CLL cells is shown in Figures 3C and 3D. The
expression of an accessory molecule ligand gene in CLL
cells and the expression of murine CD40 ligand on the
35 surface of the CLL cells is shown in Figure 3C. The

failure of the human accessory molecule ligand to be expressed on the surface of the CLL cells is shown in Figure 3D.

Figure 8 shows data from an experiment done to
5 examine whether the CD4⁺ T cells of CLL patients could be induced to express the accessory molecule ligand mRNA after CD3 ligation. An ELISA-based quantitative competitive RT-PCR was used to measure CD40 ligand transcript levels. In this experiment, CD40 ligand and
10 RNA transcribed from the CD40 ligand gene in CLL cells are compared with levels of CD40 ligand and RNA made in normal donor cells, after induction by CD3 ligation. For CD3 activation, plate coats of CD3 mAb were made and incubated with plated CLL or normal donor mononuclear
15 cells for the indicated amount of time, after which cells were analyzed for expression of surface antigens or CD154 RNA message levels. CLL or normal donor serum was added to the cells at the beginning of the activation assay for examination of modulation of CD40
20 ligand surface expression.

For quantitative CD154 RT-PCR ELISA, total RNA was extracted and competitor RNA was generated from the insert containing CD40 ligand (CD154) cDNA. Varying amounts of competitor RNA were added to separate wells
25 of isolated total RNA that subsequently were converted into cDNA. CD3 activation, ELISAs and PCR reactions were performed as described in Cantwell, M. et al., Nature Medicine 3:984-989 (1997). Biotinylated PCR products were captured onto microtiter plates (Becton
30 Dickinson, Oxnard, CA) coated with streptavidin (Sigma), and incubated. The plate was treated with NaOH to remove the sense strands and subsequently washed. The DNA was then hybridized with either wild-type gene-specific or competitor-specific oligonucleotides. Using
35 terminal transferase, each probe was labeled with a

5 molecule of digoxigenin-11-dideoxyUTP (Boehringer
Mannheim). The plate was incubated and washed with HYBE
buffer and blocking buffer, then peroxidase-conjugated
anti-digoxigenin antibody (150 U/ml; Boehringer
10 Mannheim) in blocking buffer was added. TMB
(tetramethylbenzidine) and peroxidase (Kirkegaard and
Perry Laboratories, Gaithersburg, MD) were added for
color development, and optical densities were measured
at 450 nm and Deltasoft II (Biometallics, Princeton, NJ)
15 was used for data analysis.

Standard curves plotting the moles of RNA product
versus the optical density were made for the standard
cDNA reactions. The equations describing these standard
curves were then used to calculate the moles of wild-
15 type or competitor DNA present in the unknown PCR
reactions based on the optical densities obtained in the
ELISA readings. The ratio of the quantity of wild-type
DNA to the amount of competitor DNA was then plotted
against the known quantity of competitor RNA added in
20 the initial samples. The ratio of 1 was taken for the
extrapolation of the amount of unknown moles of target
RNA in the sample (a ratio of 1 means the amount of
target RNA versus competitor RNA are equal). The
molecules of target RNA per CD4 cell was then calculated
25 based on the following formula: [(moles target CD154
RNA) x (6 X 10²³ molecules/mole) x (dilution factor of
test RNA)]/(% of CD4 T cells in total cell population).

The upper graph in Figure 8 shows that T cells of
patients with CLL do not express detectable CD40 ligand
30 after CD3 ligation. CD40 ligand RNA is produced, but it
is not stable. Although both CD40 ligand and CD40
ligand RNA are expressed in normal donor T cells (lower
graph), the levels of neither the protein or RNA are
stably maintained.

Figure 9 shows a time course for surface expression of CD40 ligand. Expression reached a peak level at 48 hours after infection and persisted at high levels for at least 6 days thereafter. In this experiment, CLL B
5 cells were infected with a gene therapy vector containing an accessory molecule ligand, at a MOI of 1000 at time zero, and then assessed by flow cytometry at various times thereafter. At each time point listed on the abscissa, the proportions of viable CLL B cells
10 that expressed detectable CD154 are indicated by the vertical bars corresponding to the percentage scale depicted on the right-hand ordinate.

15 d. Function of the Human and Murine Accessory
Molecule Ligands

i. Induction of CD80 and CD54 on Cells
Containing a Gene Therapy Vector Encoding
an Accessory Molecule

20 The CLL cells infected with the murine accessory molecule ligand gene prepared in Example 1b. were then cultured in tissue culture plates. The CLL cells were then analyzed using multiparameter FACS analysis to
25 detect induction of CD80 and CD54 expression using fluorescein isothiocyanate-conjugated monoclonal antibodies immunospecific for each of these respective surface antigens. Non-infected CLL cells were used as a control. The cells were subjected to the appropriate
30 FACS analysis and histograms were generated. CD80 mAb was obtained from Dr. Edward Clark and CD54 mAb was purchased from CALTAG Inc. The CD80 was conjugated using standard methods which have been described in Kipps et al., Laboratory Immunology II, 12:237-275
35 (1992).

The results of this analysis are shown in Figure 4A-4D. Figures 4A-4B compare the amount of CD54 expression in CLL cells which have not been transfected (Figure 4A) or CLL cells into which a gene therapy vector containing the murine CD40 ligand gene was introduced (Figure 4B). The shaded graph indicates the isotype control for FACS staining and the open graph indicates the cells stained with the anti-CD54 antibody. These results show that the level of expression of CD54 is increased in CLL cells into which the gene therapy vector containing the murine CD40 ligand was introduced.

Figures 4C and 4D compare the amount of CD80 expression in CLL cells which have not been transfected (Figure 4C) or CLL cells into which a gene therapy vector containing the murine CD40 ligand gene was introduced (Figure 4D). The shaded graph indicates the isotype control for FACS staining and the open graph indicates the cells stained with the anti-CD80 antibody. These results show that the level of expression of CD80 is increased in the CLL cells into which the gene therapy vector containing the murine CD40 ligand was introduced.

In an additional experiment, CLL cells infected with a gene therapy vector containing the murine accessory molecule ligand gene were evaluated by flow cytometry for induced expression of not only CD54 and CD80, but also CD86, CD58, CD70 and CD95. Fluorescein-conjugated mAb specific for human CD54 and CD70 were purchased from CALTAG. Fluorescein-conjugated mAb specific for human CD27, CD58, CD80, CD86, or CD95, and phycoerythrin-conjugated mAb specific for human or mouse CD40 ligand, were obtained from PharMingen. Shaded histograms represent staining of CLL B cells with FITC-conjugated isotype nonspecific mAb. In contrast to uninfected CLL cells (Figure 10, thin-lined histograms),

or Ad-lacZ-infected CLL cells (data similar to that obtained with uninfected cells, but not shown), CLL cells infected with the adenovirus vector encoding the CD40 ligand (CD154) expressed high levels of CD54 (Figure 10, top left), CD80 (Figure 10, top middle), CD86 (Figure 10, top right), CD58 (Figure 10, bottom left), CD70 (Figure 10, bottom middle), and CD95 (Figure 10, bottom right). On the other hand, CD40 ligand-CLL (CD154 CLL) expressed significantly lower levels of both surface membrane CD27 (Figure 11A, thick-lined histogram) and soluble CD27 (Figure 11B) than uninfected (Figure 11A, thin-lined histogram) ($P < 0.01$, Bonferroni t-test) or Ad-lacZ-infected CLL cells (data similar to that obtained with uninfected cells, but not shown). In the experiment shown in Figure 11A, the CLL B cells were examined for expression of CD27 via flow cytometry, three days after infection. Shaded histograms represent staining of CLL B cells with FITC-conjugated isotype control mAb. In Figure 11B, cell-free supernatants were collected, after the infection or stimulation of CLL B cells, for 72 hours and tested for the concentration of human CD27 by ELISA. The reduced expression of CD27 (Figure 11B) is similar to that noted for leukemia B cells stimulated via CD40 cross-linking with mAb G28-5 presented by CD32-expressing L cells, as described in Rassenti, L.Z. and T.J. Kipps, J. Exp. Med. 185:1435-1445.

ii. Allogeneic T Cell Responses to CLL Cells Into Which a Genetic Therapy Vector Containing a Murine CD40 Ligand Gene Has Been Introduced

The ability of CLL cells which have been infected with a gene therapy vector containing the murine CD40

ligand gene to stimulate allogeneic T cells (i.e., from another individual) was analyzed using cell proliferation assays. Briefly, the test cells were co-cultured with the genetic therapy vector containing the lac-Z gene or the murine CD40 ligand gene at a multiplicity of infection of 1,000 in the presence of IL-4 at a concentration of 10 ng/ml. In other samples, the CLL cells were stimulated with MOPC21 (a control IgG) or G28-5 (an anti-CD40 monoclonal antibody) or were preincubated on CD32-L cells and at the same time treated with IL-4. The preincubation with the CD32-L cells together with IL-4 treatment have been shown to be an efficient form of cross-linking the CD40 molecule other than direct gene transfection.

After three days of culture at 37°C, these cells were treated with mitomycin C to prevent their proliferation and then used to stimulate allogeneic T cells. Prior to this co-culture, the different aliquots of CLL cells had either been treated with the anti-CD40 monoclonal antibody or had been infected with the gene therapy vector containing either the lac-Z or murine CD40 ligand gene at a stimulator ratio of 1:10. After two days of culture at 37°C, interferon gamma (IFN γ) production was measured by ELISA assay. After five days of co-culture at 37°C, the incorporation of ³H-thymidine into replicating cells was measured after an eight hour pulse label. The results of this assay are shown in Table II below and in Figure 5.

In another experiment, CLL B cells infected with the gene therapy vector containing the CD40 ligand gene were evaluated for their ability to act as stimulator cells in an allogeneic mixed lymphocyte T cell reaction (MLTR). In parallel, the stimulatory capacity of control lac-Z-vector-infected CLL cells and CLL B cells that had been cultured with CD32-L cells and an anti-

CD40 mAb (G28-5) or an isotype control Ig, was also examined as described in Ranheim, E.A. and T.J. Kipps, J. Exp. Med., 177:925-935 (1993), Clark, E.A. and J.A. Ledbetter, Proc. Natl. Acad. Sci. USA, 83:4494-4498
5 (1986), and Banchereau, J. et al., Science 251:70-72 (1991). Effector T cells from a non-related donor were co-cultured with the CLL stimulator cells at an effector to target ratio of 4:1. After 18 h culture at 37°C, over 30% of the allogeneic CD3⁺ cells were found to
10 express the activation-associated antigen CD69 when cultured with CD154-CLL cells (data not shown). In contrast, less than 4% of the T cells expressed CD69 when co-cultured with uninfected or Ad-lacZ-infected CLL cells (data not shown).

15 Two days after the initiation of the MLTR, the concentrations of IFN γ in the culture supernatants were assayed by ELISA. The supernatants of the MLTR stimulated with CLL cells infected with the accessory molecule ligand CD40L (Figure 12A, CD154-CLL) contained
20 significantly higher levels of IFN γ (306 ± 5 ng/ml, $m \pm SE$, $n = 3$) than that of MLTR cultures stimulated with the anti-CD40 mAb (Figure 12A, α CD40-CLL) (23 ± 3 ng/ml) ($P < 0.05$, Bonferroni t-test). The latter was not significantly different from that of MLTR cultures
25 stimulated with control Ad-lacZ-infected CLL cells (Figure 12A, lacZ-CLL) (43 ± 10 ng/ml) ($P > 0.1$, Bonferroni t-test). The supernatants of effector cells alone, or of MLTR cultures stimulated with uninfected CLL cells (Figure 12A, CLL) or control Ig treated CLL
30 cells (Figure 12A, MOPC-CLL), did not contain detectable amounts of IFN γ (<2 ng/ml). Similarly, none of the leukemia B cell populations produced detectable amounts of IFN γ when cultured alone, without added effector T cells (data not shown).

After 5 days, cell proliferation was assessed by incorporation of ^3H -thymidine. Cultures with isotype control IgG-treated (Figure 12B, MOPC-CLL) or uninfected (Figure 12B, CLL) stimulator cells did not incorporate
5 more ^3H -thymidine than cultures without added leukemia-stimulator cells (Figure 12B, None). Ad-lacZ-infected CLL B cells (Figure 12B, lacZ-CLL) also were unable to stimulate allogeneic T cells to incorporate amounts of ^3H -thymidine that were much greater than that of control
10 cultures. In contrast, anti-CD40-stimulated leukemia cells or CD154-CLL cells each induced significant effector cell proliferation (Figure 12B, αCD40 -CLL or CD154-CLL) ($P < 0.05$, Bonferroni t-test). Moreover, the amount of ^3H -thymidine incorporated by cultures
15 stimulated with CD154-CLL cells ($41,004 \pm 761$ cpm ($m \pm \text{SE}$), $n = 3$) was significantly greater than that of cultures stimulated with equal numbers of αCD40 -CLL cells ($22,935 \pm 1,892$ cpm; $n = 3$) ($P < 0.05$, Bonferroni t test). However, neither of these mitomycin-C-treated
20 leukemia cell populations incorporated ^3H -thymidine when cultured without effector T cells (data not shown). Also, as described for the MLTR between allogeneic T cells and CD40-stimulated CLL cells {6549, 7167, 7168}, allogeneic T cell proliferation in response to CD154-CLL
25 could be inhibited by CTLA-4-Ig or CD11a mAb when added at the initiation of the MLTR, indicating that respective interactions between CD80/CD86 and CD28, or CD54 and CD11a/CD18, contribute to the noted allogeneic T cell reaction (data not shown).

30

Table IIAllogeneic T cell responses to CLL cells
infected with mCD40-L adenovirus

	Stimulators	<u>% positive cells</u>		<u>Allogeneic response (mean±SEM)</u>	
		mCD40-L	Human CD80	3H-TdR uptake (cpm)	IFN γ production (ng/ml)
10	None (t cells only)	-	-	3577 ± 821	n.d.*
	CLL with:				
	No activation	0	1.4	4577 ± 1097	n.d.
	MOPC21	0	1.0	5259 ± 1788	n.d.
	G28-5	0	26.7	22935 ± 1892	22.3 ± 1.6
15	lac-Z adeno	0	4.8	9037 ± 1781	43.2 ± 10.5
	mCD40-L adeno	17.5	19.7	41004 ± 761	305.7 ± 4.5

* n.d. - not detectable

iii. Stimulation of Gamma Interferon by CLL
Cells Containing an Accessory Molecule
Ligand Gene

The function of CLL cells containing an accessory molecule ligand gene (mouse CD40 ligand) was analyzed by determining the ability of those cells to activate T lymphocytes. The procedure was performed as follows: allogeneic T lymphocytes from a healthy donor (greater than 90% CD3⁺) were purified using magnetic beads and monoclonal antibodies specific for the CD14 and CD19 antigen. These allogeneic T lymphocytes then were cultured together with MMC-treated CLL cells which were infected with the accessory molecule ligand gene (murine CD40 ligand) or the lac-Z gene. This co-culture was performed in RPMI-1640 medium containing 10% fetal calf serum. After culture for 24 hours, the cells were

collected and analyzed to determine the expression of the antigen CD69 on the T lymphocytes using a standard FACS sorting protocol. The cell culture supernatants were collected after two days in culture and tested to
5 determine the concentration of human interferon gamma using an ELISA assay. A portion of the CLL cells containing an accessory molecule ligand gene (murine CD40 ligand) and a portion of the cells containing the adenovirus expressing the lac-Z were cultured in the
10 presence of human interleukin 4 IL-4 (5 ng/mL). The production of interferon gamma by allogeneic T lymphocytes in the presence of this amount of human interleukin 4 was also analyzed. The results from these analyses are shown in Figure 6.

15 As can be seen, the human CLL cells containing the accessory molecule ligand gene (murine CD40) produced substantially higher concentrations of interferon gamma in the cell culture supernatant when compared to CLL cells which contained the lac-Z gene. The increased
20 production of interferon gamma (IFN γ) by T lymphocytes exposed to CLL cells containing the accessory molecule ligand gene indicates that these CLL cells containing the accessory molecule ligand genes were effective in producing an enhanced immune response.

25

iv. Stimulation of Allogeneic T Cells Pre-Exposed to Non-Modified CLL B Cells Containing an Accessory Molecule Ligand Gene

30

Prior studies indicated that antigen presentation to T cells, in the absence of the signals derived from costimulatory molecules such as CD28, can lead to specific T cell clonal anergy. For this reason,
35 allogeneic T cells that had previously been cultured,

with non-modified CLL B cells lacking expression of CD80 and other immune accessory molecules, were tested for their ability to respond to CLL cells containing the CD40 ligand gene. Allogeneic effector cells did not
5 incorporate more ³H-thymidine in response to non-modified CLL cells (Figure 12C, CLL), or control CLL cells infected with Ad-lacZ (Figure 12C, lacZ-CLL), than when they were cultured alone (Figure 12C, None). In contrast, even after prior co-culture with non-modified
10 CLL B cells, allogeneic effector cells could still be induced to proliferate (Figure 12C, CD154-CLL) or to produce IFN γ (Figure 12D, CD154 CLL) in response to cells expressing an accessory molecule ligand. Although modest amounts of IFN γ were detected in the supernatants
15 of such secondary cultures when Ad-lacZ-infected leukemia cells were used as stimulator cells (Figure 12D, lacZ-CLL), this level was significantly lower than that noted for secondary cultures with Ad-CD40-ligand-infected CLL cells (Figure 12D, CD154-CLL) ($P < 0.05$,
20 Bonferroni t-test). Similarly, the supernatants of the leukemia cells alone (data not shown), and the effector cells alone (Figure 12D, None), of the MLTR cultures stimulated with uninfected CLL cells (Figure 12D, CLL), contained negligible amounts of IFN γ (<2 ng/ml). These
25 results indicate that allogeneic effector cells cultured with nonmodified CLL B cells are not precluded from responding to CLL B cells infected with a gene therapy vector containing the accessory molecule ligand gene.

v. Autologous T Cell Responses to CLL Cells
Into Which a Gene Therapy Vector Encoding
a Murine Accessory Molecule Ligand Gene
Has Been Introduced

5

10 T cells isolated from the blood of CLL patients
were examined for their ability to respond in vitro to
autologous CLL B cells containing a gene therapy vector
which encodes the murine accessory molecule, CD40
ligand. T cells were isolated to >95% purity, and then
co-cultured with mitomycin-C-treated autologous leukemia
cells in serum-free AIM-V medium supplemented with
exogenous interleukin-2 at 25 U/ml. Modest ³H-thymidine
incorporation ($\leq 10,000$ cpm) was detected in cultures
15 without added stimulator cells, secondary in part to the
exogenous IL-2 (Figure 13A, and data not shown). The
level of T cell proliferation, however, did not increase
in response to uninfected CLL cells (Figure 13A, CLL) or
Ad-lacZ-infected CLL cells (Figure 13A, lacZ-CLL). In
20 contrast, CLL cells infected with a gene therapy vector
containing the accessory molecule ligand (Figure 13A,
CD154-CLL) induced autologous T cells to incorporate
significantly more ³H-thymidine ($17,368 \pm 1,093$ cpm,
 $n=3$) than any of the control cultures ($P < 0.05$,
25 Bonferroni t-test). Furthermore, the MLTR stimulated
with CLL cells infected with a vector encoding an
accessory molecule ligand (CD40L) also generated
significantly more IFN γ (165 ± 3 ng/ml, $n=3$) than any of
the other cultures (Figure 13B) ($P < 0.05$, Bonferroni t-
30 test).

The T cells were harvested after 5 days from the
autologous MLTR and assessed for CTL activity against
autologous CLL B cells. T cells co-cultured with
autologous CD40-ligand-CLL cells developed CTL activity
35 for non-modified CLL B cells, effecting 40.1% lysis (\pm

2.3%) at an E:T ratio of 2:1 (Figure 13C, CD154). However, such T cells did not develop detectable CTL activity for the same target cells in the control reactions, when co-cultured with uninfected or Ad-lacZ-
5 infected CLL cells (Figure 13C).

vi. Specificity of CTL Stimulated by
Autologous CD40-Ligand-CLL B Cells for
Allogeneic CLL B Cells

10

Effector cells stimulated with autologous CD40-ligand-CLL were evaluated for their ability to secrete IFN γ or manifest CTL activity against allogeneic CLL B cells (Figure 14). After 5 days of autologous MLTR with
15 CD154-CLL or lacZ-CLL, T cells were isolated by Ficoll density gradient centrifugation, washed extensively, and then cultured in media for 24 h. Washed T cells were mixed with autologous ("Auto CLL", solid bar) or allogeneic ("Allo-1 CLL" or "Allo-2 CLL", shaded or
20 hatched bars) target CLL B cells. T cells stimulated in the autologous MLTR with CD40-ligand-CLL cells, but not with lacZ-CLL cells, produced significantly more IFN γ in response to secondary culture with non-modified autologous CLL B cells than with allogeneic CLL B cells
25 (Figure 14A) ($P < 0.05$, Bonferroni t-test). Furthermore, T cells stimulated with CD40-ligand-CLL cells, but not with lacZ-CLL cells, were cytotoxic for autologous CLL cells, but not allogeneic CLL cells (Figure 14B). Similar results were obtained with the autologous MLTR-
30 activated T cells of the allogeneic donor, again demonstrating specific cytotoxicity for autologous CLL B cells (data not shown). Finally, W6/32, a mAb to class I major histocompatibility complex (MHC I) antigens could significantly inhibit the cytotoxicity of T cells
35 stimulated with CD40-ligand-CLL cells for autologous CLL

B cells (Figure 14C, α HLA-class I)) (P < 0.05, Bonferroni t-test). Such inhibition was not observed with mAb specific for MHC class II antigen (Figure 14C, α HLA-DP), mAb specific for the Fas-ligand (Figure 14C, α FasL), or an isotype control mAb of irrelevant specificity (Figure 14C, MOPC-21). Collectively, these studies indicate that Ad-CD40-ligand-infected CLL cells can induce an autologous anti-leukemia cellular immune response in vitro, leading to the generation of MHC-class I-restricted CTL specific for autologous non-modified leukemia B cells.

e. Transactivation of Non-Infected Bystander Leukemia B Cells by Ad-CD40L CLL Cells

To address whether the changes in tumor marker expression (described in section 1di.) resulted from intracellular versus intercellular stimulation, the effect of culture density on the induced expression of CD54 and CD80 following infection with adenovirus gene therapy vector encoding the accessory molecule ligand (CD40L, or CD154) was examined. After infection, CLL cells were cultured at standard high density (e.g. 1×10^6 cells/ml) or low density (e.g. 2×10^5 cells/ml) for 3 days at 37° C. Cells plated at high density contained homotypic aggregates, whereas cells plated at low density remained evenly dispersed and without substantial cell-cell contact (data not shown). Despite expressing similar levels of heterologous CD154, CD154-CLL B cells cultured at high density were induced to express higher levels of CD54 and CD80 than CD154-CLL cells cultured at low density (Figure 15A). The stimulation achieved at high density could be inhibited by culturing the cells with a hamster anti-mouse CD154 mAb capable of blocking CD40<->CD154 interactions

(Figure 15B, α CD154 Ab). Collectively, these studies indicate that CD154-CLL cells can activate each other in *trans* and that surface expression of CD154 is necessary for optimal leukemia cell stimulation.

5 In addition, Ad-CD154-infected, uninfected, Ad-lacZ-infected, or G28-5-stimulated CLL cells were labeled with a green-fluorescence dye to examine whether CD154-CLL could stimulate non-infected bystander leukemia cells. Dye-labeled cells were used as
10 stimulator cells for equal numbers of non-labeled syngeneic CLL B cells. After 2 days' culture, stimulator cells cultured by themselves retained the green-fluorescence dye, allowing such cells to be distinguished from non-labeled CLL cells by flow
15 cytometry. Bystander (green-fluorescence-negative) CD19⁺ CLL B cells were induced to express CD54 (Figure 15C, right histogram) or CD86 (Figure 15D, right histogram) when co-cultured with Ad-CD154-infected leukemia B cells, but not with mock infected CLL cells (Figures 15C and 15D, left histograms), G28-5-stimulated CLL cells,
20 or Ad-lacZ-infected CLL cells (data not shown). As expected, these bystander (green-fluorescence-negative) CLL cells also were negative for heterologous CD154.

25 f. Treatment of Leukemia with Gene Therapy
 Vectors Encoding an Accessory Molecule Ligand

Figure 24 shows an outline for a clinical trial for testing treatment of B cell CLL with adenovirus gene
30 therapy vectors encoding modified CD40 ligand. Leukemia cells harvested by pheresis are infected with replication-defective vectors that encode the modified CD40 ligand. Following expression of this protein, the cells will be administered back to the patient for the
35 purpose of stimulating a host anti-leukemia-cell immune

response. This strategy is far superior to one that uses gene therapy to affect expression of only one immune stimulatory molecule on the leukemia cell surface. Indded, this strategy results in the leukemia cells expressing an array of immune-stimulatory accessory molecules and cytokines, as well as a molecule that can affect the same changes in leukemia cells of the patient that were never harvested.

2. Expression of Chimeric Accessory Molecule Ligand Genes

The chimeric accessory molecule ligand genes described below are prepared using standard techniques as described herein.

a. Preparation of Chimeric Accessory Molecule Ligand Genes Utilizing Domains from Two Different Accessory Molecule Genes

The human CD40 ligand gene was isolated from RNA prepared from T cells which had been activated by an anti-CD3 monoclonal antibody using 5' and 3' primers together with well known PCR methods. Chimeric accessory molecule genes of human CD40 ligand and murine CD40 ligand are constructed from the newly cloned human CD40 ligand gene and mouse CD40 ligand gene described herein as SEQ ID NO: 2. The transmembrane and cytoplasmic domains of human CD40 ligand genes are exchanged with those of the murine CD40 ligand gene and designated H(Ex)-M(Tm-Cy) CD40 ligand. These chimeric accessory molecule ligand genes are produced using the gene conversion technique described as SOEN which has been previously described by Horton, Mol. Biotechnol.,

3:93 (1995). A diagram depicting the chimeric accessory molecule ligand genes which are produced is shown in Figure 4. The nucleotide sequences of each of these respective chimeric accessory molecule ligand genes is
5 designated SEQ ID NOS: 3-7 as indicated in the Table below.

Table III

10

<u>Chimeric Accessory Molecule Ligand Gene</u>		<u>SEQ ID NO:</u>
HuIC/HuTM/MuEX CD40-Ligand		SEQ ID NO: 3
HuIC/MuTM/HuEX CD40-Ligand		SEQ ID NO: 4
15	HuIC/MuTM/MuEX CD40-Ligand	SEQ ID NO: 5
	MuIC/HuTM/HuEX CD40-Ligand	SEQ ID NO: 6
	MuIC/MuTM/HuEX CD40-Ligand	SEQ ID NO: 7

Adenovirus vectors encoding each of the chimeric
20 accessory molecules shown in Figure 2 are constructed using the methods described in Example 1. Each of these constructs are then transfected into either HeLa cells or CLL cells according to the methods of Example 1.

25 b. Expression of Chimeric Accessory Molecule Ligands on CLL and HeLa Cells

The expression of each of the chimeric accessory molecule ligand genes constructed above is analyzed by
30 using FACS analysis as specified in Example 1. The appropriate monoclonal antibody immunospecific for the external domain of either human or mouse CD40 ligand is selected and used to determine the level of expression of the chimeric accessory molecules on the surface of
35 these cells. After appropriate analysis and preparation of appropriate histograms, the expression of chimeric accessory molecules containing at least a portion of the murine CD40 ligand gene is confirmed.

c. Function of Chimeric Accessory Molecule
Ligands

CLL cells are infected with various MOI of the
5 mCD40L adenovirus and then cultured in 48 or 24 well
tissue culture plates for various times after infection
(48, 72, and 96 hours). The CD19⁺ B cells are then
analyzed by multiparameter FACS analysis for induction
of CD80 and CD54 expression using fluroescein
10 isothiocyanate-conjugated mAb specific for each
respective surface antigen as described in Example 1.
Increased amounts of CD54 and CD80 are found on cells
which have the chimeric accessory molecules containing
the domain or domains derived from the mouse CD40 ligand
15 gene.

Further analysis of the cells containing the
chimeric accessory molecule genes is carried out
according to Example 1(d). The cells containing the
chimeric accessory molecule genes which contain the
20 domains derived from the murine CD40 ligand gene are
able to stimulate the production of gamma interferon and
T cell proliferation.

d. Expression of Chimeric Accessory Molecule
25 Genes Which Contain Proximal Extracellular
Domains from Two Different Accessory Molecules
from the Same Species

A chimeric accessory molecule ligand gene is
30 prepared which contains the proximal extracellular
domain from the human CD70 gene (Domain III) with the
remainder of the domains derived from the human CD40
ligand gene. This gene is prepared using standard
biologic techniques as previously described herein.
35 This chimeric accessory molecule ligand gene has the DNA

sequence shown as SEQ ID NO: 19. A different chimeric accessory molecule ligand gene is prepared which contains the proximal extracellular domain from the murine CD40 ligand gene with the remainder of the domains derived from the human CD40 ligand gene. This gene is prepared using standard techniques as previously described herein. This chimeric accessory molecule ligand gene has the DNA sequence shown as SEQ ID NO: 20.

The chimeric accessory molecule genes shown as SEQ ID NOS: 19 and 20 are inserted into the appropriate vectors as described in Example 1 and introduced into human neoplastic cells. The expression of that chimeric accessory molecule gene in the cells is determined as was described in Example 1.

The chimeric accessory molecule encoded by each of these chimeric accessory molecule genes is found on the surface of the human neoplastic cells using the FACS analysis described in Example 1. Increased amounts of CD54 and CD80 are found on the cells containing the chimeric accessory molecule genes using the techniques described in Example 1. The cells containing the chimeric accessory molecule gene are able to stimulate the production of gamma interferon and T cell proliferation as described and assayed according to Example 1.

3. Augmentation of Vaccination Using Vectors Encoding Accessory Molecules

The following procedures were used to demonstrate the augmentation of a vaccination protocol using a gene therapy vector encoding an accessory molecule.

a. Augmentation of the Antibody Response in Mice Co-Injected with an Accessory Molecule Gene Therapy Vector and placZ

5 Three different gene therapy constructs were prepared using standard techniques including those techniques described herein. The first was a control gene therapy vector, pcDNA3, which did not contain any gene. The second, placZ, contained the Lac-Z gene which
10 encoded β -galactosidase (β -gal). The third, p-mCD40L, contained the murine CD40 ligand gene described in Example 1.

Prior to any immunizations, serum was isolated from 6-8 week old BALB/c-mice to determine the amount of any
15 initial antibodies to β -galactosidase. Each animal was injected i.m. with 100 micrograms of plasmid DNA per injection. Four separate injections were given at one week intervals.

Prior to the third injection, the animals were bled
20 to monitor the early antibody response to β -gal. One week after the final injection of plasmid DNA, the animals were bled to monitor the late antibody response to beta-galactosidase. To test the sensitivity of the assay, known amounts of anti- β -gal antibodies isolated
25 from an anti- β -gal antiserum were tested in parallel.

Serum dilutions of 1:40, 1:200, or 1:1000 were tested in an ELISA for anti- β -gal antibodies. For this, polystyrene microtiter ELISA plates were coated with β -gal at 10 microgram/ml in phosphate buffered saline.
30 The plates were washed thrice with blocking buffer containing 1% bovine serum albumin (BSA), 0.2% Tween 20 in borate buffered saline (BBS) (0.1M borate, 0.2M NaCl, pH 8.2). 50 microliters of diluted serum were added to separate wells. After at least 1 hour at room
35 temperature, the plates were washed thrice with blocking

buffer and then allowed to react with alkaline phosphatase-conjugated goat anti-mouse IgG antibody. One hour later, the plates again were washed four times with blocking buffer and incubated with 25 ml of TMB peroxidase substrate (Kirkegaard & Perry, Gaithersburg, MD). The absorbance at 405 nm of each well was measured using a microplate reader (Molecular devices, Menlo Park, CA). The higher the O.D. reading, the greater the amount of specific antibody in the sample.

10 The data for each of two experiments are provided in Tables IV and V which follow on separate sheets. The results are summarized in Tables VI and VII collating the data from the two experiments is provided as well. On the summary page n stands for the number of animals in each of the four groups. S.D. stands for standard deviation and Avg. is the average O.D. reading for all the animals in a particular group.

The results of Group 4 demonstrate that the use of a gene therapy vector encoding an accessory molecule ligand (CD40L) enhances the immunization against β -gal encoded by a genetic or gene therapy vector. The average O.D. reading of the 1:40 dilution of the sera from animals of this group is significantly higher than that of groups 1, 2, and 3 ($P < 0.05$, Bonferroni t tests, see Table VII).

Data from an additional experiment further reinforce the finding that the gene therapy vector encoding an accessory molecule ligand enhances immunization against β -gal (Figure 16). Here, pCD40L and placZ were co-injected into skeletal muscle, to test for enhancement of the immune response to placZ, a pCDNA3-based vector encoding *E. coli* β -galactosidase. The relative anti- β -gal Ab activities were determined via ELISA. As expected, mice injected with either the non-modified pCDNA3 vector or pCD40L alone did not

produce detectable antibodies to β -gal (Figure 16A). Mice were injected with either 100 μ g pCDNA3 (checkered bar), 50 μ g pCDNA3 + 50 μ g pCD40L (lined bar), 50 μ g pCDNA3 + 50 μ g placZ (striped bar), or 50 μ g pCD40L + 50 μ g placZ (solid bar). On the other hand, mice that received placZ and pCDNA3 developed detectable anti- β -gal antibodies one week after the fourth and final injection, at d28. Mice that received placZ and pCD40L developed higher titers of anti- β -gal antibodies than mice injected with placZ and pCDNA3. Figure 16B, ELISA analyses of serial dilutions of sera collected at d28, shows that mice co-injected with placZ and pCD40L had an eight-fold higher mean titer of anti- β -gal antibodies at d28 than mice treated with placZ + pCDNA3.

i. Immunoglobulin Subclass Production
Stimulated by Accessory Molecule Vector
Co-Injection

Despite enhancing the titer of the anti- β -gal antibody response, the subclass of anti- β -gal IgG induced by injection of placZ was not altered by the co-injection of pCD40L. IgG_{2a} anti- β -gal antibodies predominated over IgG₁ subclass antibodies in the sera of mice injected with either placZ and pCDNA3 or placZ and pCD40L (Figure 17). Also depicted are the ELISA O.D. measurements of anti- β -gal IgG₁ and anti- β -gal IgG_{2a} present in the pre-immune sera (striped bar) or post-immune sera (solid bar), collected at d28) of each group of mice, injected as indicated on the abscissa. In contrast, BALB/c mice injected with β -gal protein developed predominantly IgG₁ anti- β -gal antibodies, and no detectable IgG_{2a} anti- β -gal antibodies.

ii. Augmentation of Vaccination by Accessory
Molecule Vector Requires Co-Injection
with placZ at the Same Site

5 The adjuvant effect of the pCD40L plasmid on the
anti- β -gal antibody response was noted only when it was
injected into the same site as placZ (Figure 18).
Groups of BALB/c mice (n=4) received intramuscular
injections of placZ and pCD40L together at the same
10 site, or as simultaneous separate injections at distal
sites (right and left hind leg quadriceps). A control
group received intramuscular injections of placZ and
pcDNA3 at the same site. Animals were bled at d28 and
the sera tested for anti- β -gal Ab at different
15 dilutions, as indicated on the abscissa. The graph
illustrates a representative experiment depicting the
mean O.D. at 405 nm of replicate wells of each of the
serum samples for each group, at a 1:40, 1:200, or
1:1000 dilution. Animals injected simultaneously with
20 placZ and pCD40L, but at different sites, did not
develop detectable anti- β -gal antibodies until d28.
Moreover, the anti- β -gal antibody titers of the sera
from such animals at d28 were similar to that of mice
that received placZ and pcDNA3, and significantly less
25 than that of animals that received placZ and pCD40L
together at the same site.

iii. Augmentation of Vaccination When
Accessory Molecule Vector and placZ are
30 Co-Injected into Dermis

The pCD40L plasmid also enhanced the anti- β -gal
antibody response to placZ when injected into the
dermis. In the experiment shown in Figure 19, mice
35 received intradermal injections, near the base of the

tail, with either 50 μ g pCDNA3 (checkered bar), 25 μ g pCDNA3 + 25 μ g pCD40L (lined bar), 25 μ g pCDNA3 + 25 μ g placZ (striped bar), or 25 μ g pCD40L + 25 μ g placZ (solid bar). Injections, bleeds and ELISA analyses were
5 performed as in Figure 16A. The checkered bar and lined bar groups each consisted of 8 mice while the striped bar and solid bar groups each consisted of 12 mice. The height of each bar represents the mean O.D. of sera at a 1:40 dilution of each group \pm S.E. A statistical
10 analysis of the data indicated that the striped bar and solid bar groups are independent ($P < .05$). As observed with intramuscular injection, mice co-injected with placZ and pCD40L developed detectable serum anti- β -gal antibodies one week following the second injection
15 (d14), and two weeks earlier than mice injected with placZ and pCDNA3. Moreover, these animals also had an eight-fold higher mean titer of anti- β -gal antibodies than mice of the placZ-injected group at d28. Mice injected with either the non-modified pCDNA3 vector or
20 pCD40L alone did not produce detectable antibodies to β -gal.

25 b. Augmentation of the CTL Response in Mice Co-Injected with an Accessory Molecule Gene Therapy Vector and placZ

The ability of pCD40L to enhance induction, by placZ, of CTL specific for syngeneic β -gal-expressing target cells was tested. BALB/c mice co-injected with
30 pCD40L and placZ into skeletal muscle (Figure 20A) or dermis (Figure 20B) generated greater numbers of CTL specific for P13.2, a placZ transfected P815 cell line, than mice co-injected with placZ and pCDNA3. At a 5:1 effector:target ratio, the splenocyte effector cells
35 from mice that received intramuscular injections of

placZ and pCD40L achieved greater than 20% specific lysis of P13.2. In contrast, when splenocytes of mice that received the control injection with placZ and pCDNA3 were used, a 9-fold greater ratio of effector to target cells was required to achieve this level of specific lysis. Similarly, the splenocyte effector cells from mice that received intradermal injections of placZ and pCD40L killed more than 50% of the P13.2 cells at effector:target ratios of 4:1. To achieve comparable levels of specific lysis required eight-fold higher effector:target ratios using splenocytes from mice that received intradermal injections of placZ and pCDNA3. Nevertheless, the splenocytes of mice co-injected with pCD40L and placZ did not have greater non-specific CTL activity for P815 cells than that of mice that received placZ along with pCDNA3 (Figure 20). As expected, the splenocytes from mice that received injections of pCDNA3 alone, or pCDNA3 and pCD40L, did not mediate specific lysis of P13.2 or P815 cells.

20

Table IV

Experiment #1 Injections of plasmid DNA i.m.: 4/3/96; 4/10/96; 4/17/96; 4/24/96

ELISA for anti-beta galactosidase

5	antibodies: Group	Animal	Dilution of Pre-Bleed (4/3)			Dilution of Bleed (4/17)		
			1/140	1/200	1/1000	1/140	1/200	1/1
10	pcDNA3 (p-control, 100 mcg) (Control vector)	1	0.09	0.11	0.09	0.06	0.06	
		2	0.11	0.09	0.09	0.07	0.07	
		3	0.12	0.11	0.10	0.09	0.09	
		4	0.11	0.10	0.10	0.08	0.11	
		Avg.	0.11	0.11	0.11	0.11	0.11	
		S.D.	0.01	0.01	0.01	0.01	0.02	
15	p-lacZ (50 mcg) + p-Control (50 mcg)	5	0.13	0.10	0.10	0.07	0.11	
		6	0.10	0.11	0.10	0.07	0.06	
		7	0.19	0.10	0.18	0.07	0.07	
		8	0.10	0.09	0.10	0.08	0.07	
		Avg.	0.13	0.10	0.12	0.07	0.08	
		S.D.	0.04	0.01	0.04	0.01	0.02	
20	p-lacZ (50 mcg) + pRcCMV-mCD40L (p-mCD40L, 50 mcg)	27	0.06	0.06	0.06	0.13	0.11	
		18	0.06	0.06	0.06	0.27	0.13	
		19	0.06	0.06	0.06	0.23	0.19	
		20	0.06	0.06	0.06	0.23	0.19	
		Avg.	0.06	0.06	0.06	0.74	0.47	
		S.D.	0.00	0.00	0.00	1.06	0.66	

Table V

Experiment #2 Injections of plasmid DNA i.m.: 6/5/96; 6/12/96; 6/19/96; 6/26/96

Dilutions of sera for anti-beta

	Animal	Dilution of Pre-Bleed (6/5)			Dilution of Bleed (7/1)		
		1/140	1/200	1/1000	1/140	1/200	1/1
5	galactosidase antibodies:						
	Group						
	p-Control (50 mcg)	9	0.02	0.02	0.06	0.04	0.01
	+	10	0.06	0.02	0.10	0.02	0.02
	p-mCD40L (50 mcg)	11	0.02	0.02	0.07	0.03	0.01
10		12	0.06	0.03	0.05	0.18	0.04
	Avg.		0.04	0.04	0.04	0.04	0.04
	S.D.		0.02	0.01	0.02	0.07	0.01
15	p-lacZ (50 mcg)	5	0.02	0.03	0.02	0.06	0.04
	+	6	0.03	0.02	0.03	0.14	0.03
	p-Control (50 mcg)	7	0.56	0.13	0.06	0.29	0.06
		8	0.01	0.02	0.05	0.06	0.02
	Avg.		0.15	0.05	0.04	0.13	0.04
	S.D.		0.27	0.05	0.02	0.11	0.02
20	p-lacZ (50 mcg)	13	0.23	0.06	0.05	0.28	0.07
	+	14	0.02	0.02	0.03	0.04	0.02
	p-mCD40L (50 mcg)	15	0.02	0.02	0.02	0.89	0.21
		16	0.05	0.04	0.02	0.11	0.04
25	Avg.		0.08	0.04	0.03	0.33	0.08
	S.D.		0.10	0.02	0.02	0.39	0.09

Table VI

Summary		Pre-Immune @ beta-gal			Early @ beta-ga		
		1/140	1/200	1/1000	1/140	1/200	1/1
5	1) p-Control (n = 4)	Avg. 0.11	0.11	0.11	0.11	0.11	
		S.D. 0.01	0.01	0.01	0.01	0.02	
10	2) p-mCD40L + p-Control (n = 4)	Avg. 0.04	0.04	0.04	0.04	0.04	
		S.D. 0.02	0.01	0.02	0.07	0.01	
	3) p-lacZ + p-Control (n = 8)	Avg. 0.11	0.04	0.04	0.11	0.03	
		S.D. 0.22	0.04	0.01	0.09	0.02	
15	4) p-lacZ + p-mCD40L (n = 8)	Avg. 0.11	0.04	0.03	0.25	0.06	
		S.D. 0.10	0.02	0.01	0.32	0.07	
Anti-beta-galactosidase standard:		67 ng	22ng	7.4ng	2.5ng	.82ng	.27ng
20	O.D.	3.01	2.98	2.05	1.10	0.52	0.26
		3.14	3.14	2.25	1.20	0.56	0.26

Table VII

BONFERRONI t-TESTS

5	Comparison	Difference of means			t	P<.05
	4 vs 2:	2.06 -	0.04 =	2.02	3.782	Yes
	4 vs 1:	2.06 -	0.11 =	1.95	3.651	Yes
	4 vs 3:	2.06 -	0.61 =	1.45	3.325	Yes
	3 vs 2:	0.61 -	0.04 =	0.57	1.067	No
10	3 vs 1:	0.61 -	0.11 =	0.50	Do not test	
	1 vs 2:	0.11 -	0.04 =	0.07	Do not test	

Degrees of freedom: 20

15

ONE WAY ANALYSIS OF VARIANCE

	Group	N	Mean	Std Dev	SEM
	1	4	0.11	0.01	0.00
20	2	4	0.04	0.04	0.02
	3	8	0.61	1.11	0.39
	4	8	2.06	0.97	0.34
	5	4	1.51	0.77	0.38
	6	4	1.14	0.53	0.26
25	7	4	0.83	0.43	0.22

ONE WAY ANALYSIS OF VARIANCE

	Source of Variation	SS	DF	Variance Est (MS)
30	Between Groups	18.29	6	3.05
	Within Groups	18.39	29	0.63
	Total	36.69	35	

$$\begin{array}{rclclclclcl}
 & & s2_bet & & MSbet & & 3.05 & & & & \\
 35 & F & = & \frac{\quad}{s2_wit} & = & \frac{\quad}{Mswit} & = & \frac{\quad}{0.63} & = & 4.81 & P = 0.002
 \end{array}$$

4. Treatment of Neoplasia Using a Gene Therapy Vector Containing an Accessory Molecule Gene or Chimeric Accessory Molecule Gene

5 a. Treatment of Neoplasia in Mice

The treatment of a neoplasia in a mouse model system has been demonstrated using the genes encoding accessory molecule ligands of the present invention.

10 Gene therapy vectors containing an accessory molecule ligand gene (murine CD40 ligand) were prepared as has been previously described in the above examples. These gene therapy vectors were used to introduce that accessory molecule ligand gene into neoplastic cells,

15 Line1 cells, from a tumor which originated in BALB/c mice. The accessory molecules were introduced into the neoplastic cells according to the above examples. The expression of the accessory molecule ligand on the surface of these neoplastic cells was confirmed using

20 flow cytometry as has been described in the above examples.

The effectiveness of the accessory molecule ligand genes for treating neoplasia was shown as follows. Female BALB/c mice (6-8 weeks old) were injected i.p.

25 with 1.0×10^5 irradiated Line1 neoplastic cells. The neoplastic Line1 cells are derived from a spontaneous lung adenocarcinoma in a BALB/c mouse. This neoplastic cell has been described by Blieden et al., Int. J. Cancer Supp., 6:82 (1991). Other female BALB/c mice

30 were injected i.p. with 1.0×10^5 irradiated Line1 tumor cells that had previously been transduced with the gene therapy vector encoding the accessory molecule ligand gene (murine CD40) as described above.

Each group of mice was allowed to generate an

35 immune response for 10 days. After 10 days each mouse

was challenged with 1.0×10^4 live, non-irradiated Line1
neoplastic cells. These mice were then monitored for
the formation of tumors and then sacrificed when the
tumors grew to 2.0 cm because of morbidity. The results
5 of this monitoring are shown in Figure 7. As can be
seen by Figure 7, the mice immunized with the neoplastic
cell expressing the accessory molecule ligands of the
present invention on the cell surface remained free of
tumor throughout the experiment. Mice immunized with
10 the neoplastic cells not having the accessory molecule
ligand genes of the present invention succumbed to tumor
50 days after challenge with the neoplastic cells.

Figure 21 demonstrates downmodulation of human
CD40L, but not murine CD40L, in lung tumor cell lines
15 that express CD40. Human cell lines HeLa (CD40-negative
cervical carcinoma, Figure 21A), A427 (CD40-negative
lung carcinoma, Figure 21B), NCI 460 (weakly CD40-
positive lung large cell carcinoma, Figure 21C), and SK-
Mes-1 (strongly CD40-positive lung squamous cell tumor,
20 Figure 21D) were infected with adenovirus encoding lac-Z
(Ad-LacZ), murine CD40L (Ad-mCD40L), and human CD40L
(Ad-hCD40L) at an MOI of 0 (Blank), 1, and 10. 48 hours
after infection, murine CD40L and human CD40L surface
expression was determined. The percentage of cells that
25 express ligand are plotted on the Y-axis. Human and
mouse CD40L are expressed at equal levels in CD40-
negative cell lines. However, only murine CD40L
expression is stable on cell lines that express CD40.
In contrast to mCD40L, human CD40L is downmodulated on
30 CD40-positive tumors.

The data graphed in Figure 22A show that CD40
binding induces expression of tumor surface markers.
Treating CD40-expressing lung cancer cell lines with
 α CD40 mAb resulted in enhanced expression of the tumor
35 cell surface markers CD95 (Fas), CD54 (ICAM-1) and class

I major histocompatibility antigens (MHC I). NCI 460, a weakly CD40-positive lung large cell carcinoma, was incubated with a CD40-specific monoclonal antibody (thick line), or MOPC21, an isotype control mAb (thin line), on CD32-expressing mouse fibroblasts for 48 hours. Following the 48 hr incubation, the lung tumor cells were analyzed for CD95, CD54, and MHC-I expression by FACS.

Figure 22B again shows downmodulation of human CD40L by CD40-positive tumor cells. HeLa (CD40-negative), CLL (CD40-positive), and SK-MES-1 (CD40-positive) tumor cells were cocultured for 24 hours with CD3-activated normal donor T cells at a tumor cell:T cell ration of 2.5:1. Following coculture, CD2-expressing T cells were analyzed for CD40L surface expression by FACS. Thin lines represent T cells stained with FITC-labeled isotype control antibody (MOPC21) and thick lines represent activated T cells stained with FITC-labeled α CD40L antibody (α CD154 antibody). The CD40-positive tumor cell lines, SK-MES-1, and CLL, do not express CD40 ligand on their surfaces.

5. Expression of the Human and Mouse Accessory Molecule Ligand, Fas Ligand, in Human Blood Lymphocytes

a. Construction of a Genetic Construct and Gene Therapy Vector Containing the Human and Mouse Fas Ligand Gene

Either the human accessory molecule ligand gene (human Fas ligand) or the murine accessory molecule ligand gene (murine Fas ligand) was constructed utilizing the respective human and murine genes.

An altered accessory cell molecule, in which a putative MMP-cleavage site was removed, was made and designated ΔFasL-pcDNA3. The nucleotide sequence of ΔFasL-pcDNA3 is listed as SEQ ID NO: 40. Human Fas ligand

5 nucleotides 325 to 342, encoding six amino acids, are missing from ΔFasL. The design of ΔFasL was based on reasoning that Domain III contains sites most accessible to MMPs, and could thus be the target on the molecule for cleavage from the surface of the cell. Sequences of

10 the human Fas ligand gene have been determined and are listed as SEQ ID NOS: 13 and 30 (Genbank accession U11821). Sequences of mouse Fas ligand genes have been determined and are listed as SEQ ID NOS: 14 (C57BL/6, Genbank accession U10984) and 31 (Balb/c, Genbank

15 accession U58995). The sequence of the rat Fas ligand gene has been determined and is listed as SEQ ID NO: 25 (Genbank accession U03470). Chimeric constructs are made, as described in Example 2 for CD40 ligand chimeric constructs, in which Domain III of human Fas ligand is

20 replaced with Domains of other proteins, particularly proteins of the TNF family. Chimeric constructs include, but are not limited to, human Fas ligand with Domain III replaced by Domain III of murine Fas ligand (chimeric sequence listed as SEQ ID NO: 37, sequence

25 line-up shown in Figure 37), or replaced by Domain III of human CD70 (chimeric sequence listed as SEQ ID NO: 38, sequence line-up shown in Figure 38), or replaced with Domain I of human CD70 (chimeric sequence listed as SEQ ID NO: 39, sequence line-up shown in Figure 39).

30 Chimeric constructs in which multiple domains, for example, two copies of human CD70 Domain III, are inserted into human Fas ligand in place of Domain III, are also made using methods described in Example I. Chimeric constructs in which synthetic sequences are

used to replace Domain III of human Fas ligand are also made.

i. Human Fas Ligand Cloning

5

The cDNA encoding human Fas-ligand was subcloned in the eukaryotic expression vector pcDNA3. Normal donor blood lymphocytes were activated for 4 hours with 1 ng/ml PMA plus 0.5 uM ionomycin. Total RNA was isolated with the Qiagen Rneasy kit. cDNA was then synthesized from poly-A RNA with oligo-dT primers using the Gibco-BRL Superscript cDNA synthesis kit. The gene encoding human Fas-ligand was then PCR amplified with the Fas-ligand-specific primers (sense primer, SEQ ID NO: 32, antisense primer, SEQ ID NO: 33). The Fas-ligand PCR product was then subcloned into pcDNA3 using standard molecular biology techniques. RT-PCR products, subcloned into pcDNA3, are designated hFasL-pcDNA3.

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ii. Murine Fas Ligand Cloning

The murine Fas-ligand genes from Balb/c and C57/BL6 strains of mice were also amplified following activation of mouse splenocytes with PMA plus ionomycin as described above, and amplified from poly-A synthesized cDNA as described above (sense primer, SEQ ID NO: 34, antisense primer, SEQ ID NO: 35). These genes were subcloned in the pTARGET expression vector (Promega, Madison, WI). RT-PCR products, subcloned into pcDNA3, are designated mFasL-pcDNA3.

25
30

iii. Adenovirus Vector Construction

For construction of adenovirus vectors encoding human Fas-ligand, murine Fas-ligand or Δ Fas-ligand, the

cloned cDNA insert is subcloned into the plasmid pRC/RSV (Invitrogen, San Diego, CA) at the HindIII-XbaI site. A BglII-XhoI fragment with the RSV promoter-enhancer and the bovine growth hormone poly-A signal sequence was
5 subcloned into the BamHI-XhoI site of plasmid MCS(SK)pXCX2. The plasmid MCS(SK)pXCX2 is a modification of the plasmid pXCX2, in which the pBluescript polylinker sequence was cloned into the E1 region. The resulting plasmid then is co-transfected along with pJM17 into 293
10 cells using the calcium phosphate method. Isolated plaques of adenovirus vectors are picked and expanded by infecting 293 cells. High titer adenovirus preparations are obtained, as described above which uses a cesium chloride gradient for concentrating virus particles via a
15 step gradient, with the densities of 1.45g/cm³ and 1.20g/cm³, in which samples are centrifuged for 2 hours in an SW41 rotor (Beckman, Brea, CA) at 25,000 rpm at 4° C. The virus band is desalted using a Sephadex G-25 DNA grade column (Pharmacia, Piscataway, NJ), and the
20 isolated virus is stored at -70° C in phosphate-buffered saline with 10% glycerol. The titer of the virus is determined by infecting permissive 293 cells at various dilutions and counting the number of plaques. Titers typically range from 10¹⁰ to 10¹² plaque forming units/ml.
25 The adenovirus constructs are designated Ad-hFasL, Ad-mFasL and Ad-ΔFasL.

b. Introduction of the Murine and Human Fas Ligand Genes into Human Cells

30

The constructs hFasL-pcDNA3, mFasL-pcDNA3 and ΔFasL-pcDNA3 are transfected into 293 via electroporation. The transfected cells are selected in medium containing G418. Fas-ligand transfectants are screened for expression of
35 the transgene using anti-Fas-ligand antibody and flow

cytometry. The methods used are similar to those described for transfection of CD40L into CLL cells.

For FasL-adenovirus infection, 10^6 freshly thawed and washed CLL cells or HeLa cells are suspended in 0.5 to 1 mL of culture medium for culture at 37°C in a 5% CO₂-in-air incubator. Adenovirus are added to the cells at varying multiplicity of infection (MOI), and the infected cells are cultured for 48 hours, unless otherwise stated, before being analyzed for transgene expression.

10

c. Expression of the Fas Ligand Genes in Human Cells

Mice with the lymphoproliferative or generalized lymphoproliferative disorder are unable to delete activated self-reactive cells outside of the thymus. This is related to the fact that, in these mice, interactions between the Fas receptor and an accessory molecule ligand, Fas ligand, are defective. These animals develop numerous disorders including lymphadenopathy, splenomegaly, nephritis, and systemic autoimmune pathology which resembles that seen in patients with systemic lupus erythematosus or rheumatoid arthritis (RA). It is conceivable that the normal interactions between the Fas receptor and the accessory molecule ligand that are responsible for clearance of activated lymphocytes from joints may be impaired in RA patients.

RA synovial lymphocytes express the Fas receptor at a higher proportion than that of matched RA blood lymphocytes to matched normal donor blood lymphocytes. On the other hand, RA synovial lymphocytes express little or no accessory molecule ligand. Since the RA synovial lymphocytes are sensitive to Fas-induced apoptosis, it is feasible that local expression of Fas ligand in the RA

joint could serve to eliminate the synovial mononuclear cells that potentially mediate RA autoimmune pathology.

Figure 23 shows that Fas-ligand expression in lymphocytes is inhibited by exposure to RA synovial fluid. Normal donor blood T cells were activated for 5 hours with 1 ng/ml PMA plus 0.5 μ M ionomycin. Cells were incubated in the presence of rheumatoid arthritis blood plasma (circles), RA synovial fluid (diamonds), or neither (squares). In addition, cells were incubated with increasing concentrations of the MMP inhibitor BB94. Following activation, cells were analyzed for Fas-ligand surface expression by FACS. The percentage of cells expressing Fas ligand are plotted in Figure 23. This experiment demonstrates that there is a factor(s) present in RA synovial fluid and serum that prevents surface expression of Fas-ligand.

d. Function of Human, Murine and Chimeric
Accessory Molecule Ligand, Fas Ligand

To determine the capacity of the Δ FasL constructs, the above-mentioned transfected cells are mixed with the Fas-ligand sensitive human T cell line, JURKAT. Following 4 hours coculture, the nonadherent JURKAT cells are collected and evaluated for apoptosis. The fluorescent compound 3,3' dihexyloxacarbocyanine iodide (DiOC₆) is used to evaluate for apoptosis using a modification of a previously described protocol. For this, the cells are washed once at room temperature in phosphate buffered saline (PBS, pH 7.2). Cells are placed into separate wells of a 96 well U-bottom plastic microtiter plate at 10^5 - 5×10^5 cells/well in 50 μ l total volume. If indicated, saturating amounts of PE-conjugated antibodies are added followed by addition of

DiOC₆ and propidium iodide (PI). DiOC₆ and PI are used at 40 nM and 10 ng/ml final concentrations, respectively. The cells are then incubated 15 minutes in a 37°C, 5% CO₂ tissue culture incubator. The stained cells are then washed twice in ice cold PBS and ultimately suspended in 200 ml SM and analyzed by FACS. Dead cells and debris with characteristic forward and light scatter profiles and PI staining are excluded from analysis.

The ability of cells expressing ΔFasL-pcDNA3 to direct Fas-mediated apoptosis of cells expressing CD95 is compared with that of cells expressing FasL-pcDNA3. Relative stability of the protein products encoded by ΔFasL-pcDNA3 or FasL-pcDNA3 pre- and post- culture with RA synovial fluid, and with or without the metalloproteinase inhibitors, are assessed via flow cytometry of cells expressing either ligand.

6. Treatment of Arthritis with Gene Therapy Vectors Encoding an Accessory Molecule Ligand, Fas Ligand

The heterologous Fas-ligand constructs, made as described above, that show the highest stability of expression in combination with the greatest ability to mediate Fas-induced apoptosis, are used in gene therapy for RA. Potential therapeutic constructs are tested in well-characterized mouse models of arthritis to assess efficacy and function *in vivo*.

a. Gene Therapy Treatment of Arthritis in Mice

i. Mouse Models for Arthritis

One mouse arthritis model is collagen-induced arthritis. It is known that injecting DBA/1 mice with type II collagen in complete Freund's adjuvant (CFA)

induces an arthritis with synovitis and erosions that histologically resemble RA. For our studies, male DBA/I mice are immunized with bovine type II collagen in complete Freund's adjuvant on day 0 and boosted
5 intraperitoneally (i.p.) on day 21. On day 28, animals are given an additional i.p. injection with lipopolysaccharide (LPS) and/or the same type collagen, or an injection of acetic acid alone. Swelling and/or redness of a fore or hind paw in animals immunized with
10 collagen typically is detected the third or fourth week following the second injection. The vertebrae are only rarely affected, and then only weeks after the initial peripheral joint swelling. Affected joints display initial histologic changes of synovial edema, followed by
15 synovial hyperplasia.

Another animal model, recently described by Kouskoff, V. et al., in Cell 87:811-822 (1997) was generated fortuitously, by crossing a T cell receptor (TCR) transgenic mouse line with the non-obese-diabetic
20 (NOD) strain to produce the KRN x NOD mouse model of RA. The offspring of such a mating universally develop a joint disease that is highly similar to that of patients with RA. Moreover, the disease in these animals has an early and reproducible time of onset and a highly
25 reproducible course. The arthritis apparently is induced by chance recognition of an NOD-derived major histocompatibility complex (MHC) class II molecule by the transgenic TCR, leading to breakdown in the general mechanisms of self-tolerance and systemic self-
30 reactivity.

ii. Relief of Arthritis Symptoms in Mice
Treated with a Gene Therapy Vector
Encoding an Accessory Molecule Ligand

5 We have adapted and modified a protocol originally described by Sawchuk and colleagues for micro-injecting adenovirus vectors into mouse joints. Using this procedure we can reproducibly inject a 5 μ l volume into the articular space of the mouse knee. In this
10 procedure, the mice are anesthetized with metofane. A small incision of approximately 2-3 mm is made with a #11 scalpel blade in the skin over the lateral aspect of the knee to visualize the patello-tibial ligament. We can inject up to 5 μ l of fluid using a micro-100 μ l-Hamilton
15 syringe and a 30-gauge needle. After the injection, the knee incision is closed with Nexabond (Veterinary Products Laboratory). Our adenovirus titers typically exceed 10^{10} plaque forming units (pfu) per ml, making it possible to deliver at least 5×10^8 pfu of virus in 5 ml
20 into the knee joints, as outlined above. Control animals are injected with control Ad-lacZ vector, a replication-defective adenovirus vector lacking a transgene, or with the buffer used to suspend the virus (10 mM Tris, 1 mM $MgCl_2$, 10% glycerol).

25 In another method, splenocytes will be harvested from mice that are syngeneic to the host animal intended for adoptive transfer of transduced cells. Cell proliferation will be induced with exogenous IL-12 (100 units/ml) for 48 h. Cells are counted and then re-plated
30 at densities of 5×10^5 or 1×10^6 cells per ml in a 12-well dish with 1 ml complete culture medium per well. Virus and ConA are added together at the time of re-plating in the presence of polybrene (8 μ g/ml). The medium is changed 24 hours after infection with complete
35 medium containing 100 units of recombinant IL-2 per ml.

Aliquots of the transduced cells are examined, for Fas-ligand expression, at 48 hours after infection via flow cytometry.

Animals will receive standardized numbers of
5 cytokine-producing cells or control mock-transfected cells intraperitoneally. Concentrated cell suspensions are injected directly into the mouse synovium, as described in section 4A above. In parallel, aliquots of the transferred cell populations are maintained in tissue
10 culture supplemented with exogenous IL-2.

Mice are monitored in a blinded fashion for signs of arthritis. The date of disease onset is recorded and clinical severity of each joint or group of joints (toes, tarsus, ankle, wrist, knee) are graded as follows: 0
15 (normal), 1 (erythema), 2 (swelling), 3 (deformity), 4 (necrosis). The scores are summed to yield the arthritic score. The severity of arthritis is expressed both as the mean score observed on a given day, and as the mean of the maximal arthritic score reached by each mouse
20 during the clinical course of the disease. At the time of death, hind paws are dissected free and processed for histologic examination or for RT-PCR. The histologic severity of the arthritis is scored on a scale of 0-3 for synovial proliferation and inflammatory cell
25 infiltration, where a score of 0 = normal and 3 = severe.

For mice receiving intra-synovial injection of control of test adenovirus vector, the level of arthritis observed between contralateral sites is compared. In addition, the overall joint score minus that of the
30 injected joint for the entire animal is compared with that observed in the joint injected with the control or test adenovirus vector.

Local administration of Fas-ligand adenovirus expression vectors will result in clearance of activated
35 cells, as assessed by measuring the relative levels of

CD80 mRNA by quantitative RT-PCR. This treatment also will lead to an enhanced level. Also, whether such level of apoptosis identified in affected mouse synovial tissue is assessed by the TUNEL assay ("Terminal
5 deoxynucleotidyl transferase (TdT)-mediated dUTP Nick End Labeling"). TUNEL is performed by immersing the sections in TdT buffer (30 mM Tris-HCl, pH 7.2, 140 nM sodium cacodylate, 1 mM cobalt chloride), and then adding TdT (GIBCO BRL, Grand Island, NY) and biotinylated dUTP
10 (Boehringer Mannheim, Indianapolis, IN). The reaction is terminated by immersing the sections in TB buffer (300 mM sodium chloride, 30 mM sodium citrate). Subsequently, the samples are treated with peroxidase-labeled streptavidin and then visualized using the VECTASTAIN ABC
15 kit (Vector Laboratories Inc., Burlingame, CA). For immunohistochemistry, the sections are blocked with 4% skim milk for 30 minutes at room temperature, then incubated with biotinylated mAbs specific for mouse CD3, B220, CD80, or CD95 (Fas). These antibodies are
20 available from Pharmingen (San Diego, CA).

b. Treatment of Rheumatoid Arthritis Patients with
a Gene Therapy Vector Encoding an Accessory
Molecule Ligand, Fas Ligand

25

Candidate Fas-ligand constructs identified as having potential therapeutic benefit are used in human protocols to treat RA. Human protocols encompass either *in vivo* or *ex vivo* methods to deliver the Fas-ligand constructs.
30 Furthermore, the Fas-ligand constructs are potentially delivered by either viral or non-viral methods. Outlines of therapeutic strategies are described below.

An *ex vivo* therapy is similar to a protocol described for intra-articular transplantation of
35 autologous synoviocytes retrovirally transduced to

synthesize interleukin-1 receptor antagonist (Evan, Christopher et. al., Clinical Trial to Assess the Safety, Feasibility, and Efficacy of Transferring a Potentially Anti-Arthritic Cytokine Gene to Human Joints with
5 Rheumatoid arthritis, Human Gene Therapy, Vol. 7, 1261-1280). In this procedure, after clinical diagnosis of RA, the synovium is harvested during total joint replacement. The synoviocytes re-isolated and expanded, then transduced or transfected with heterologous Fas-
10 ligand into synoviocytes (via retrovirus, adenovirus, naked DNA, etc.). The gene-modified synoviocytes are then reinjected into the patient, who is monitored and tested for amelioration of RA-associated symptoms, and for expression and function of the Fas-ligand in modified
15 synoviocytes.

In another ex vivo protocol, an allogeneic immortalized cell line that stably expresses the heterologous Fas-ligand is administered to the RA patient. In this protocol, a stable immortalized cell
20 line expressing Fas-ligand (introduced by transfection of the gene into the cell by nonviral methods, such as electroporation), or by viral transduction of the gene into the cell) is constructed. The modified cell line is injected into the patient, who is monitored and tested
25 for amelioration of RA associated symptoms, and for expression and function of the hFas-ligand in modified synoviocytes.

An in vivo based therapy will is similar in concept to the amelioration of collagen-induced-arthritis using a
30 murine Fas-ligand adenovirus gene therapy vector, described in Zhang, et al., J. Clin. Invest. 100:1951-1957 (1997). In our use of such an approach, delivery of the hFas-ligand construct or chimeric Δ fasL directly to the joints of RA patients is performed using either viral
35 or non-viral methods. In this procedure, the Fas-ligand

construct (e.g. hFas-ligand adenovirus) is directly injected into the synovium. Patients are monitored and tested for amelioration of RA-associated symptoms as well as biological testing for expression and function of the

5 hFas-ligand in modified synoviocytes.

2025-10-27 14:00:00

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: Kipps, Thomas J.
Sharma, Sanjai
Cantwell, Mark

(ii) TITLE OF INVENTION: NOVEL EXPRESSION VECTORS
CONTAINING ACCESSORY
MOLECULE LIGAND GENES AND
THEIR USE FOR IMMUNOMODULA-
TION AND TREATMENT OF
MALIGNANCIES AND AUTOIMMUNE
DISEASE

(iii) NUMBER OF SEQUENCES: 35

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(E) COUNTRY: U.S.A.
(F) ZIP: 90071-2066

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5" Diskette,
1.44 Mb storage
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: IBM P.C. DOS 5.0
(D) SOFTWARE: FastSeq Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/132145
(B) FILING DATE: 12/9/96

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Guise, Jeffrey W.
(B) REGISTRATION NUMBER: 34,613
(C) REFERENCE/DOCKET NUMBER: 231/003

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(C) TELEX: 67-3510

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 786 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 783 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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TGA

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(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 783 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	786 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single
(D)	TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	783 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single
(D)	TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

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GAAGATTTTG	TATTCATAAA	AAAGCTAAAG	AGATGCAACA	AAGGAGAAGG	ATCTTTATCC	240

TTGCTGAACT	GTGAGGAGAT	GAGAAGGCAA	TTTGAAGACC	TTGTCAAGGA	TATAACGTTA	300
AACAAAGAAG	AGAAAAAAGA	AAACAGCTTT	GAAATGCAAA	GAGGTGATGA	GGATCCTCAA	360
ATTGCAGCAC	ACGTTGTAAG	CGAAGCCAAC	AGTAATGCAG	CATCCGTTCT	ACAGTGGGCC	420
AAGAAAGGAT	ATTATACCAT	GAAAAGCAAC	TTGGTAATGC	TTGAAAATGG	GAAACAGCTG	480
ACGGTTAAAA	GAGAAGGACT	CTATTATGTC	TACACTCAAG	TCACCTTCTG	CTCTAATCGG	540
GAGCCTTCGA	GTCAACGCCC	ATTCATCGTC	GGCCTCTGGC	TGAAGCCCAG	CATTGGATCT	600
GAGAGAATCT	TACTCAAGGC	GGCAAATACC	CACAGTTCCT	CCCAGCTTTG	CGAGCAGCAG	660
TCTGTTCACT	TGGGCGGAGT	GTTTGAATTA	CAAGCTGGTG	CTTCTGTGTT	TGTCAACGTG	720
ACTGAAGCAA	GCCAAGTGAT	CCACAGAGTT	GGCTTCTCAT	CTTTTGGCTT	ACTCAAATC	780
TGA						783

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	786 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single
(D)	TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

ATGATAGAAA	CATACAGCCA	ACCTTCCCCC	AGATCCGTGG	CAACTGGACT	TCCAGCGAGC	60
ATGAAGATTT	TTATGTATTT	ACTTACTGTT	TTTCTTATCA	CCCAGATGAT	TGGGTCAGCA	120
CTTTTGTGCTG	TGTATCTTCA	TAGAAGGTTG	GACAAGATAG	AAGATGAAAAG	GAATCTTCAT	180
GAAGATTTTG	TATTCATGAA	AACGATACAG	AGATGCAACA	CAGGAGAAAAG	ATCCTTATCC	240
TTACTGAACT	GTGAGGAGAT	TAAAAGCCAG	TTTGAAGGCT	TTGTGAAGGA	TATAATGTTA	300
AACAAAGAGG	AGACGAAGAA	AGAAAACAGC	TTTGAAATGC	AAAAAGGTGA	TCAGAATCCT	360
CAAATTGCGG	CACATGTCAT	AAGTGAGGCC	AGCAGTAAAA	CAACATCTGT	GTTACAGTGG	420
GCTGAAAAAG	GATACTACAC	CATGAGCAAC	AACTTGGTAA	CCCTGGAAAA	TGGGAAACAG	480
CTGACCGTTA	AAAGACAAGG	ACTCTATTAT	ATCTATGCCC	AAGTCACCTT	CTGTTCCAAT	540
CGGGAAGCTT	CGAGTCAAGC	TCCATTTATA	GCCAGCCTCT	GCCTAAAGTC	CCCCGGTAGA	600
TTGAGAGAGAA	TCTTACTCAG	AGCTGCAAAT	ACCCACAGTT	CCGCCAAACC	TTGCGGGCAA	660
CAATCCATTC	ACTTGGGAGG	AGTATTTGAA	TTGCAACCAG	GTGCTTCGGT	GTTTGTCAAT	720
GTGACTGATC	CAAGCCAAGT	GAGCCATGGC	ACTGGCTTCA	CGTCCTTTGG	CTTACTCAAA	780
CTCTGA						786

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	786 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single
(D)	TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ATGATAGAAA	CATACAGCCA	ACCTTCCCCC	AGATCCGTGG	CAACTGGACT	TCCAGCGAGC	60
ATGAAGATTT	TTATGTATTT	ACTTACTGTT	TTCCTTATCA	CCCAAATGAT	TGGATCTGTG	120
CTTTTTGCTG	TGTATCTTCA	TAGAAGGTTG	GACAAGATAG	AAGATGAAAG	GAATCTTCAT	180
GAAGATTTTG	TATTCATGAA	AACGATACAG	AGATGCAACA	CAGGAGAAAAG	ATCCTTATCC	240
TTACTGAACT	GTGAGGAGAT	TAAAAGCCAG	TTTGAAGGCT	TTGTGAAGGA	TATAATGTTA	300
AACAAAGAGG	AGACGAAGAA	AGAAAACAGC	TTTGAAATGC	AAAAAGGTGA	TCAGAATCCT	360
CAAAATTGCGG	CACATGTCAT	AAGTGAGGCC	AGCAGTAAAA	CAACATCTGT	GTTACAGTGG	420
GCTGAAAAAG	GATACTACAC	CATGAGCAAC	AACTTGGTAA	CCCTGGAAAA	TGGGAAACAG	480
CTGACCGTTA	AAAGACAAGG	ACTCTATTAT	ATCTATGCCC	AAGTCACCTT	CTGTTCCAAT	540
CGGGAAGCTT	CGAGTCAAGC	TCCATTTATA	GCCAGCCTCT	GCCTAAAGTC	CCCCGGTAGA	600
TTCGAGAGAA	TCTTACTCAG	AGCTGCAAAT	ACCCACAGTT	CCGCCAAACC	TTGCGGGCAA	660
CAATCCATTC	ACTTGGGAGG	AGTATTTGAA	TTGCAACCAG	GTGCTTCGGT	GTTTGTCAAT	720
GTGACTGATC	CAAGCCAAGT	GAGCCATGGC	ACTGGCTTCA	CGTCCTTTGG	CTTACTCAAA	780
CTCTGA						786

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	864 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single
(D)	TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

AACTCTAACG	CAGCATGATC	GAAACATACA	GTCAACCTTC	TCCCCGCTCC	GTGGCCACTG	60
GACCACCTGT	CAGTATGAAA	ATTTTTATGT	ATTTACTTAC	AGTTTTTCTT	ATCACCCAGA	120
TGATTGGGTC	AGCGCTTTTT	GC'TGTGTATC	TTCACAGACG	ATTGGACAAG	ATAGAAGACG	180
AAAGGAATCT	TCATGAAGAT	TTTGTGTTCA	TGAAAACGAT	ACAGAGATGC	AATAAAGGAG	240
AGGGGTCCTT	ATCCTTACTG	AACTGTGAGG	AAATTAGAAG	CCGGTTTGAA	GACTTGGTCA	300
AGGATATAAT	GCAAAACAAA	GAAGTAAAGA	AGAAAGAAAA	AACTTTTGAA	ATGCACAAGG	360
GTGATCAGGA	GCCTCAGATA	GCGGCACATG	TCATCAGTGA	GGCCAGTAGT	AAAACAACCT	420
CTGTTCTCCA	GTGGGCCCCC	AAAGGATACT	ACACCCTAAG	CAACAACCTG	GTAACCCCTG	480
AAAACGGGAA	ACAGCTGGCC	GTGAAAAGAC	AAGGATTCTA	TTACATCTAC	ACCCAAGTCA	540
CCTTCTGTTC	CAATCGGGAA	ACTTTGAGTC	AAGCTCCATT	TATAGCCAGC	CTCTGCCTGA	600
AGTCCCCAAG	TGGATCAGAG	AGAATCTTAC	TGAGAGCTGC	AAACACCCAC	AGTTCTTCCA	660
AACCATGCGG	GCAGCAATCC	ATTCACCTAG	GAGGAGTCTT	TGAATTGCAA	TCGGGTGCTT	720
CGGTGTTTGT	CAATGTGACT	GATCCAAGTC	AAGTGAGCCA	CGGGACGGGC	TTCACATCAT	780
TTGGCTTACT	CAAACCTCTGA	ACGGTGTAAG	CCAGCAGGCT	GCGGCTGGGC	TGATGCTGGT	840
GGTCTTCACA	ATCCAGGAAA	GCAG				864

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3634 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GAATTCCGGG	TGATTTCAC	CCCGGCTGTC	CAGGCTTGTC	CTGCTACCCC	ACCCAGCCTT	60
TCCTGAGGCC	TCAAGCCTGC	CACCAAGCCC	CCAGCTCCTT	CTCCCCGCAG	GACCCAAACA	120
CAGGCCTCAG	GACTCAACAC	AGCTTTTCCC	TCCAACCCGT	TTTCTCTCCC	TCAACGGACT	180
CAGCTTTCTG	AAGCCCCCTC	CAGTTCTAGT	TCTATCTTTT	TCCTGCATCC	TGTCTGGAAG	240
TTAGAAGGAA	ACAGACCACA	GACCTGGTCC	CCAAAAGAAA	TGGAGGCAAT	AGGTTTTGAG	300
GGGCATGGGG	ACGGGGTTCA	GCCTCCAGGG	TCCTACACAC	AAATCAGTCA	GTGGCCCAGA	360
AGACCCCCCT	CGGAATCGGA	GCAGGGAGGA	TGGGGAGTGT	GAGGGGTATC	CTTGATGCTT	420
GTGTGTCCCC	AACTTTCCAA	ATCCCCGCCC	CCGCGATGGA	GAAGAAACCG	AGACAGAAGG	480
TGCAGGGCCC	ACTACCGCTT	CCTCCAGATG	AGCTCATGGG	TTTCTCCACC	AAGGAAGTTT	540
TCCGCTGGTT	GAATGATTCT	TTCCCCGCCC	TCCTCTCGCC	CCAGGGACAT	ATAAAGGCAG	600
TTGTTGGCAC	ACCCAGCCAG	CAGACGCTCC	CTCAGCAAGG	ACAGCAGAGG	ACCAGCTAAG	660
AGGGAGAGAA	GCAACTACAG	ACCCCCCTG	AAAACAACCC	TCAGACGCCA	CATCCCCTGA	720
CAAGCTGCCA	GGCAGGTTCT	CTTCCTCTCA	CATACTGACC	CACGGCTTCA	CCCTCTCTCC	780
CCTGGAAAGG	ACACCATGAG	CAGTGAAAGC	ATGATCCGGG	ACGTGGAGCT	GGCCGAGGAG	840
GCGCTCCCCA	AGAAGACAGG	GGGGCCCCAG	GGCTCCAGGC	GGTGCTTGTT	CCTCAGCCTC	900
TTCTCCTTCC	TGATCGTGGC	AGGCGCCACC	ACGCTCTTCT	GCCTGCTGCA	CTTTGGAGTG	960
ATCGGCCCCC	AGAGGGAAGA	GGTGAGTGCC	TGGCCAGCCT	TCATCCACTC	TCCCACCCAA	1020
GGGGAAATGA	GAGACGCAAG	AGAGGGAGAG	AGATGGGATG	GGTGAAAGAT	GTGCGCTGAT	1080
AGGGAGGGAT	GAGAGAGAAA	AAAACATGGA	GAAAGACGGG	GATGCAGAAA	GAGATGTGGC	1140
AAGAGATGGG	GAAGAGAGAG	AGAGAAAGAT	GGAGAGACAG	GATGTCTGGC	ACATGGAAGG	1200
TGCTCACTAA	GTGTGTATGG	AGTGAATGAA	TGAATGAATG	AATGAACAAG	CAGATATATA	1260
AATAAGATAT	GGAGACAGAT	GTGGGGTGTG	AGAAGAGAGA	TGGGGGAAGA	AACAAGTGAT	1320
ATGAATAAAG	ATGGTGAGAC	AGAAAGAGCG	GGAAATATGA	CAGCTAAGGA	GAGAGATGGG	1380
GGAGATAAGG	AGAGAAGAAG	ATAGGGTGTC	TGGCACACAG	AAGACACTCA	GGGAAAGAGC	1440
TGTTGAATGC	TGGAAGGTGA	ATACACAGAT	GAATGGAGAG	AGAAAACCAG	ACACCTCAGG	1500
GCTAAGAGCG	CAGGCCAGAC	AGGCAGCCAG	CTGTTCCCTC	TTTAAGGGTG	ACTCCCTCGA	1560
TGTTAACCAT	TCTCCTTCTC	CCCAACAGTT	CCCCAGGGAC	CTCTCTCTAA	TCAGCCCTCT	1620
GGCCCAGGCA	GTCAGTAAGT	GTCTCCAAAC	CTCTTTCTTA	ATTCTGGGTT	TGGGTTTGGG	1680
GGTAGGGTTA	GTACCGGTAT	GGAAGCAGTG	GGGGAAATTT	AAAGTTTTTG	TCTTGGGGGA	1740
GGATGGATGG	AGGTGAAAGT	AGGGGGGTAT	TTTCTAGGAA	GTTTAAGGGT	CTCAGCTTTT	1800
TCTTTTCTCT	CTCCTCTTCA	GGATCATCTT	CTCGAACCCC	GAGTGACAAG	CCTGTAGCCC	1860
ATGTTGTAGG	TAAGAGCTCT	GAGGATGTGT	CTTGGAACCT	GGAGGGCTAG	GATTTGGGGA	1920
TTGAAGCCCG	GCTGATGGTA	GGCAGAACTT	GGAGACAATG	TGAGAAGGAC	TCGCTGAGCT	1980
CAAGGGAAGG	GTGGAGGAAC	AGCACAGGCC	TTAGTGGGAT	ACTCAGAACG	TCATGGCCAG	2040
GTGGGATGTG	GGATGACAGA	CAGAGAGGAC	AGGAACCGGA	TGTGGGGTGG	GCAGAGCTCG	2100
AGGGCCAGGA	TGTGGAGAGT	GAACCGACAT	GGCCACACTG	ACTCTCCTCT	CCCTCTCTCC	2160
CTCCCTCCAG	CAAACCCTCA	AGCTGAGGGG	CAGCTCCAGT	GGCTGAACCG	CCGGGCCAAT	2220
GCCCTCCTGG	CCAATGGCGT	GGAGCTGAGA	GATAACCAGC	TGGTGGTGCC	ATCAGAGGGC	2280

CTGTACCTCA	TCTACTCCCA	GGTCCTCTTC	AAGGGCCAAG	GCTGCCCCCTC	CACCCATGTG	2340
CTCCTCACCC	ACACCATCAG	CCGCATCGCC	GTCTCCTACC	AGACCAAGGT	CAACCTCCTC	2400
TCTGCCATCA	AGAGCCCCTG	CCAGAGGGAG	ACCCAGAGG	GGGCTGAGGC	CAAGCCCTGG	2460
TATGAGCCCA	TCTATCTGGG	AGGGGTCTTC	CAGCTGGAGA	AGGGTGACCG	ACTCAGCGCT	2520
GAGATCAATC	GGCCCCACTA	TCTCGACTTT	GCCGAGTCTG	GGCAGGTCTA	CTTTGGGATC	2580
ATTGCCCTGT	GAGGAGGACG	AACATCCAAC	CTTCCCAAAC	GCCTCCCCTG	CCCCAATCCC	2640
TTTATTACCC	CCTCCTTCAG	ACACCCTCAA	CCTCTTCTGG	CTCAAAAAGA	GAATTGGGGG	2700
CTTAGGGTCG	GAACCCAAGC	TTAGAACTTT	AAGCAACAAG	ACCACCACTT	CGAAACCTGG	2760
GATTTCAGGAA	TGTGTGGCCT	GCACAGTGAA	GTGCTGGCAA	CCACTAAGAA	TTCAAACCTGG	2820
GGCCTCCAGA	ACTCACTGGG	GCCTACAGCT	TTGATCCCTG	ACATCTGGAA	TCTGGAGACC	2880
AGGGAGCCTT	TGGTTCTGGC	CAGAATGCTG	CAGGACTTGA	GAAGACCTCA	CCTAGAAATT	2940
GACACAAGTG	GACCTTAGGC	CTTCCTCTCT	CCAGATGTTT	CCAGACTTCC	TTGAGACACG	3000
GAGCCCAGCC	CTCCCCATGG	AGCCAGCTCC	CTCTATTTAT	GTTTGCACCT	GTGATTATTT	3060
ATTATTTTATT	TATTATTTAT	TTATTTACAG	ATGAATGTAT	TTATTTGGGA	GACCGGGGTA	3120
TCCTGGGGGA	CCCAATGTAG	GAGCTGCCTT	GGCTCAGACA	TGTTTTCCGT	GAAAACGGAG	3180
CTGAACAATA	GGCTGTTCCC	ATGTAGCCCC	CTGGCCTCTG	TGCCTTCTTT	TGATTATGTT	3240
TTTTAAATA	TTTATCTGAT	TAAGTTGTCT	AAACAATGCT	GATTTGGTGA	CCAACCTGTCA	3300
CTCATTGCTG	AGCCTCTGCT	CCCCAGGGGA	GTTGTGTCTG	TAATCGCCCT	ACTATTCACT	3360
GGCGAGAAAT	AAAGTTTGCT	TAGAAAAGAA	ACATGGTCTC	CTTCTTGGA	TTAATTCTGC	3420
ATCTGCCTCT	TCTTGTGGGT	GGGAAGAAGC	TCCCTAAGTC	CTCTCTCCAC	AGGCTTTAAG	3480
ATCCCTCGGA	CCCAGTCCCA	TCCTTAGACT	CCTAGGGCCC	TGGAGACCCT	ACATAAACAA	3540
AGCCCAACAG	AATATTCCCC	ATCCCCCAGG	AAACAAGAGC	CTGAACCTAA	TTACCTCTCC	3600
CTCAGGGCAT	GGGAATTTC	AACCTCTGGA	ATTC			3634

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1997 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GAGACAGAGT	CTTGCTCTGT	CCCCAGGCT	GGAATACAGT	GGTGCGATCT	TGACTCACTG	60
CAGCCTCCGC	CTCCCAGGTT	CAAATAATTC	TCCAGCCTCA	GCCTCCCGAG	TAGCTGGGAC	120
TGCAGATGCG	CACCAGCACG	CCTGGCTAAT	TTTTGTATTT	ATTATAGAGA	TGGGGTTTCA	180
CCATGTTGGC	CAGCTGGTCT	CAAACCTCCTG	ACCTCAAGTA	ATCCGCCCAC	CTCAGACTCC	240
CAAAGTGCCA	GGATTACAGG	TGTGAGCCAC	TGCACCAGGC	CTGGAACAAT	TTTAAAATAA	300
TGTATTGGCT	CTGCAAATGC	AGCTTCAGAA	CAAGTCCCTT	AGCTGTCCCC	ACCCACCCCT	360
AAGTCACCAC	CCTTAAGCCT	CACCCATGTG	GAATTCTGAA	ACTTCCTTTG	TAGAAAACCTT	420
TGGAAGGTGT	CTGCCACATT	GATCCTGGAA	TGTGTGTTTA	TTTGGGGTTA	TATAAATCTG	480
TTCTGTGGAA	GCCACCTGAA	GTCAGGAAGA	GATGGAGGGC	ATCCTTCAGG	AGTGAGATGA	540
GACCTCATCA	TACTTGACTG	TCCAGCATCA	TCTCTGAGTA	AGGGGACCAA	AAAATTTATC	600
TTCCAAACTA	GGACACTTTC	AAGAGTGGAA	GGGGGATCCA	TTAATATTTT	CACCTGGACA	660

AGAGGCAAAC	ACCAGAATGT	CCCCGATGAA	GGGGATATAT	AATGGACCTT	CTTGATGTGA	720
AACCTGCCAG	ATGGGCTGGA	AAGTCCGTAT	ACTGGGACAA	GTATGATTTG	AGTTGTTTGG	780
GACAAGGACA	GGGGTACAAG	AGAAGGAAAT	GGGCAAAGAG	AGAAGCCTGT	ACTCAGCCAA	840
GGGTGCAGAG	ATGTTATATA	TGATTGCTCT	TCAGGGAACC	GGGCCTCCAG	CTCACACCCC	900
AGCTGCTCAA	CCACCTCCTC	TCTGAATTGA	CTGTCCCTTC	TTTGGAAGTC	TAGGCCTGAC	960
CCCACTCCCT	GGCCCTCCCA	GCCCACGATT	CCCCTGACCC	GACTCCCTTT	CCCAGAACTC	1020
AGTCGCCTGA	ACCCCCAGCC	TGTGGTTCTC	TCCTAGGCCT	CAGCCTTTCC	TGCCTTTGAC	1080
TGAAACAGCA	GTATCTTCTA	AGCCCTGGGG	GCTTCCCCGG	GCCCCAGCCC	CGACCTAGAA	1140
CCCGCCCGCT	GCCTGCCACG	CTGCCACTGC	CGCTTCCTCT	ATAAAGGGAC	CTGAGCGTCC	1200
GGGCCCAGGG	GCTCCGCACA	GCAGGTGAGG	CTCTCCTGCC	CCATCTCCTT	GGGCTGCCCC	1260
TGCTTCGTGC	TTTGGACTAC	CGCCAGCAG	TGTCCTGCCC	TCTGCCTGGG	CCTCGGTCCC	1320
TCCTGCACCT	GCTGCCTGGA	TCCCCGGCCT	GCCTGGGCCT	GGGCTTGGTG	GGTTTGGTTT	1380
TGGTTTCCTT	CTCTGTCTCT	GACTCTCCAT	CTGTCACTCT	CATTGTCTCT	GTCACACATT	1440
CTCTGTTTCT	GCCATGATTC	CTCTCTGTTC	CCTTCCTGTC	TCTCTCTGTC	TCCCTCTGCT	1500
CACCTTGGGG	TTTCTCTGAC	TGCATCTTGT	CCCCTTCTCT	GTCGATCTCT	CTCTCGGGGG	1560
TCGGGGGGTG	CTCTCTCCCA	GGGCGGGAGG	TCTGTCTTCC	GCCGCGTGCC	CCGCCCCGCT	1620
CACTGTCTCT	CTCTCTCTCT	CTCTTTCTCT	GCAGGTTCTC	CCCATGACAC	CACCTGAACG	1680
TCTCTTCTCT	CCAAGGGTGT	GTGGCACCAC	CCTACACCTC	CTCCTTCTGG	GGCTGCTGCT	1740
GGTTCTGCTG	CCTGGGGCCC	AGGTGAGGCA	GCAGGAGAAT	GGGGGCTGCT	GGGGTGGCTC	1800
AGCCAAACCT	TGAGCCCTAG	AGCCCCCTC	AACTCTGTTC	TCCCCTAGGG	GCTCCCTGGT	1860
GTTGGCCTCA	CACCTTCAGC	TGCCCAGACT	GCCCCGTCAGC	ACCCCAAGAT	GCATCTTGCC	1920
CACAGACCC	TCAAACCTGC	TGCTCACCTC	ATTGGTAAAC	ATCCACCTGA	CCTCCCAGAC	1980
ATGTCCCCAC	CAGCTCT					1997

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10240 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GAATTCCCCG	GATCAAAGTC	AGCATTAAT	CCCAGTTTAG	GTTTTGAGGC	TAAGTTCAAG	60
TTTGAGTCTA	ATGTCATTTT	AGCCTTGTTT	GGAGGACTCA	GAGATTTTAC	TAGTTTCTCC	120
GCAGAGACCA	CTGTAGAAAC	TGCATTTCCC	TGAGTTTGG	GCACAAGACT	CCAGTCATCA	180
CCCCTCCCAC	ACAGGGAAAG	CCCCAAACCA	ACTGCTGGCC	TCCTCAAGAA	AGAAACCGAA	240
TTTACACAA	CCTCCGAAAC	TAAGATTGAA	ACCAAGATTG	GCCCATCTCA	AGGCGCGTCC	300
TCCAGCACAT	TGAGAATGTC	GCTGATGGAG	CCTCGGCCCA	GCTCTCGAGC	TTCTTCTCTT	360
TCTGTCTCTC	ATGTCTTCTC	ATCACTCCTT	CTCACCTTCC	CGTTTTTGTG	CTGCAATGCC	420
CCCTTCTTCC	TCTCTTCTCT	GGGTTTTTCC	CTTTATTTCT	CACTGTACCA	TTTTATATTT	480
TAATAAAGCC	GAGGTCTCCT	AGTCCATCAG	CTCCTACTGT	TGGAGAGGAG	GCAGAAAGAA	540
ACAGCAGGAC	GGCAAAGGGA	CTCCAGAGAA	AGAGACTCAG	AGGAAAGGCA	AGAAACAGGG	600
ACCAAGAGAG	AGGCCAACAG	TGACACAAGA	CACAGTGAGG	TTAAAAGAAA	TAAGATGAGG	660
CCAAGATAGA	GACCAAGCTA	TTTAAAAGAG	CCATCTGTGG	CTACCTTCT	TCCGCCATCG	720
CATCTGGTCA	GCCACCAAGA	TTTTGCCTAG	AAACGTTTCT	CCTCTCCATT	CTCCTGCTGC	780

TGCTGCTGCT	GCTGCTGCTG	CTGCTGCTGC	TGCTGCTGCT	GCTGCTGCTG	CTGCCTTAAT	840
ACGAATGCAG	GCTCTTGTCA	TCTCCTTGCT	GGGTGTGTGC	AAAATCCTCC	TAAGTGGTCT	900
CCACACTTCT	CATTTCCCTT	CCAGCCCCCT	ATCTTCCATA	CTTCCATTTA	TTTATTTTGG	960
CCATGCCCCAT	GGCATGTGGC	AGTTCCAGGG	GCCAGGGATC	AAACCTGTGC	CAATGCAGTG	1020
ACCGTGTGAG	ATCCTTAACC	CACTGCACAC	AAGGCAACGC	CCCTCGAGTC	ATTCTCATTT	1080
TTTAAATATA	CCAATTTGAG	GGGGTCCCTC	TTTCACTTAA	AAATTTTGGC	AGCTCCCTAT	1140
CATGATGAGA	AGGAATTCCA	AACCATTTTT	CTTGTGTGCA	AACCCTTCAG	CATGTGTCTT	1200
CAGCTTACTT	CCCAAGCCTC	ATCCCTGCTC	CTTCTACGTG	TACCCATGTG	TACATCTCCA	1260
CACACCATAT	ACTCTTTTTT	ACCTCCCATC	TTTGCACCTT	CTGTTCCCTC	TCTCTGCCCC	1320
TCACCATCTT	TTTTGCTTTG	ATACTTAATG	CCTCTCCCTC	AGGCCAGGTT	CAATGGCTTT	1380
TCTGTGGGCT	GCTTTAAGCC	CACTGTGATG	GAACCTTATCA	CATTTTATTT	TATTTGACTT	1440
TCTTTTTTAGG	GCCGCACCCA	GCATATGGAG	ATTCCCAGGC	TAGGGATCTA	ATCGGAGCTG	1500
TATCTGCCAG	CCTGCGCTGG	AGCCACAGCA	ACGTGGGATC	CGAGCCTGAG	GGGTTTTGAT	1560
GTCCTGTGGC	ACAGAAGTTA	CATTTCAGGCT	GTGCATGAAC	TATTTCTCCT	GTTCTCCTCC	1620
CCCTGCTTGA	GGCCCTGCAG	CTTTGCCTCT	CATGCCTTGC	TGCTCTGACC	TATGACTTCT	1680
TTTTGTTTTGC	ATTCCATCTC	TTTAGTTTTT	TCTCTGTTCC	ACAAACATTT	ACTGAGCATC	1740
TACATGAGGC	ATTGAGGATA	CGGATGGGAA	AGACAGTCCC	CTGACCTCTG	GGACCTCAAA	1800
GACCAATTGT	GGAAGACTGG	TTGGTTATCA	GATAATTACA	ATGAAGTGTG	GGAGTCCCTG	1860
TCATGGGTCA	GCAGGTAATG	AACCCAGTAA	ACGATCCATG	AGGATGCAGA	TTCAATCCCT	1920
GGCCTTGCTC	AGCGGGTTAA	GGATCCAGCG	TTCCCACAAG	CTGTGGTGTG	GGTCGCAGAT	1980
GCGACTCAGA	TCTTGCAATT	CTGTGGCTGT	GGTGTAGGCT	GGTGGCTACC	CCTAGCCTGG	2040
GAACCTCCAT	ATGCCTCAGG	TGCGGCCCTA	AAAGACAAAA	AAAAAAAAGA	GAGAACTTTT	2100
TCTTTTTCTT	AATGTGTAAC	CTACAAGCTA	AGTGAAAACT	GGCTCCTATT	CCATAACGTT	2160
TGTATCATTT	TTCATACTAG	CCAAATACTA	GAACACGGGA	GTTCCCGTCG	TGGTGCAGCA	2220
GAAACAAATT	CGACTAGGAA	CCATGAGGTT	GCGGGTTTCG	TCCCTGGCCT	TGCTCAGTGG	2280
GTTAAGGATG	CGGCGTTGCC	GTGAGCTGTG	GTGTAGGTCG	CAGATGTGGC	TCGGATCTAG	2340
TGTTGCTGTG	GCTCTGGTGT	AGGCCGGCAG	CAACAGCTCT	GATTAGACTC	CTAGCCTGAG	2400
AACCTCCATA	AGCTGTGGCT	GCGGCCCTAT	AAAGACAAAA	AAAAAAAAAA	GGCCAAATAC	2460
TAGAAACAAA	CCAAATGCCC	ATCAACAGAA	GAATAGATAA	GTTAATTGGG	GTATATGCAC	2520
ACAATAGCAT	CACACAATAA	CATGCACACA	ATAACATCAC	AATGAAATAA	AAATTACTAC	2580
TGACAGACAC	AACCATATAG	ATGAATTTCA	CAAACACAAC	AGCGAGAATA	AAAGCCAAGC	2640
ACAGATGAGT	TGTCTGTGTG	GATTCAATTC	TATGAAGTTC	AAGCGCAGGA	AGAACTTAAT	2700
CTATAGTGAC	AGAGGTCAGA	GAGCAGTTGG	TTGTCTTTGG	CAGGTATGAA	CTGGGAGTGG	2760
GCATGAGAGA	ACTTTCTGGA	GACCTAAAAA	TATATTGGAC	TGGATGGTGG	CAACATGGCT	2820
ACAAGAAGAT	GGAAAAGTTC	CTCAGGCTGT	CCACTTGGGA	GACGGGCTTC	TCACGGGACC	2880
TAAGTTCTGC	ATCAGCAGAG	GGGGAAATCC	TTAATGATTT	GACAATTACA	AAGTGTATTG	2940
GCTTTACCGA	TGTATTTTCA	ACACAATCCC	TCTGCTGTCC	CCACCCACC	CTAGGTCACC	3000
ACCCTTAAGC	TCCACCTGTG	TGGAATTTCT	AAGCCTCCCC	TGTAGAGAAC	TTTAGCAGTT	3060
GCCACGTTCT	TTTGATGCAG	GAACGTGTTG	TCTAGAGTTA	GACACATCTG	ATCTGTGGGG	3120
CCCACCCAAG	GTTGGGACAT	GGTGGGGGGC	GGCCTTCTGC	AGTGAGATGA	AACCTCATTT	3180
TAGGTGATTT	CGTGGCCTCA	TCCCTGAGTC	AGATCTTCCA	AATGAGGACA	CTTTGGAGAG	3240
CAAAAGGGGG	CTCCCTGAAG	ATTTCCCTCCA	GGACAGCAGG	AACAAACCAG	GATGTCCCAG	3300
GCAGGAGGGT	ATAGAAGGGA	ACTTGTTGAT	ATGAAATCAG	CCAGATGACC	TGGAAAATAC	3360
ACAGACTGGG	ACAAGTGTGA	CTTGAGCCTC	TTGGGCCCCAG	GACAGGGGTA	CAGAGGAGGA	3420
AACGTGCACA	GAGAGAAGCC	CGTAATCAGC	CAAGGCTGCA	GAGGTGTTAT	ACATAATCGC	3480
TCTTCACGCA	ACCGGGCAAG	CAGCCCACGC	CCCAGCTGCA	CTCCATCTCC	TCCTCTGAAC	3540
TCACCGTCCC	TTCTCTGGAA	CTCCTAAGCC	TGACCCCGCT	CCCTGGCCCT	CCCAGCCCAC	3600
GGTTCCCCTG	ACCCCACTCC	CTTTCCCAGA	ACTCAGTCAT	CTGAGCCCCC	AGCCTGCGTT	3660
CTCTCCTAGG	CCTCAGCCTT	TCCTGCCTTC	GCGTGAAACA	GCAGCATCTT	CTAAGCCCTG	3720

GGCTTCCCCA	GGCCCCAGCC	CCGGCCTAGA	ACCCGCCCAG	CCGACCTGCC	CACGCTGCCA	3780
CTGCCGGCTT	CCTCTATAAA	GGGACCCAGG	GCGCCCAGAA	AGGGGCCCAC	AGGGGTCCCG	3840
CACAGCAGGT	GAGACTCTCC	CACCCCATCT	CCTAGGGCTG	TCCGGGTGCT	GGACTCCCCC	3900
CTCACTTCGG	TCCCTCCGCC	CGCTCCCCTG	CCTTCCTGCC	CCTCCTGCAT	CTTCACCCCG	3960
GCCTGGGCCT	TGGTGGGTTT	GGTTTTGGTT	TGTTCTCTCT	GATTCTTTAT	CTGTCAGGCT	4020
CTTTCTAGCT	CTCACACACT	CTGATCCCTC	TCTGTTCCCT	TCCCATCTCT	GTTTCTCTCT	4080
GGGTCTCCCC	CTGCTCACCT	CGGGATTTCC	CTGAGTGCCT	CTGGTCCCCT	TCTCTGTCTG	4140
GCGCCCCGTC	TCTTGTCTCT	CGGGGTGGCT	GTCTCCGAGG	GCAGGAGGCC	TTCTTCCGCA	4200
GGTGCCCCGC	CCCCTCACT	GTCTCTCTCC	CCCCACAGGT	TTTCCCCATG	ACACCACCTG	4260
GACGCCTCTA	CCTCCGGAGG	GTGTGCAGCA	CCCCATCCT	CCTCCTCCTG	GGGCTGTCTG	4320
TGGCCCTGCC	GCCCGAGGCC	CAGGTGAGGC	AGCAGGAGAG	CGGGCCGTGG	GGGCAGCCTT	4380
CGCCAACCTT	GGGCCTCAGA	GCCTCTCTGA	CGCTCTTCTC	CCCTAGGGGC	TCCCTGGCGT	4440
CGGCCTCCCA	CCCTCAGCTG	CACAGCCTGC	CCATCAGCAC	CCCCCAAAGC	ACTTGGCCAG	4500
AGGCACCCTC	AAACCTGCCG	CTCACCTCGT	TGGTAAACAT	CCACCTGGCC	TCCCAGACCT	4560
GTAGCCCCCA	GTCTCTCTCC	TATGCCCCCT	CTTCAGGGAC	TGAAGCATCC	CTCCCCCCCCA	4620
TCTCCCCCCA	CCCCCTAAAT	GGAGGCATCC	CACTCCCCGAC	TCCCTCCCCAA	CCATCCCCCA	4680
GGAACTCAGT	CCAGCACCTG	CTTCCTCAGG	GATTGAGACC	TCCGACCCCC	AGGTCTTTGA	4740
CTCCCAACCC	CTCTGGCTCT	TCCTAGGAGA	CCCCAGCACC	CCGGACTCAC	TGCGCTGGAG	4800
AGCGAACACG	GATCGTGCCT	TCCTCCGCCA	TGGCTTCTTG	CTGAGCAACA	ACTCCCTGCT	4860
GGTCCCCACC	AGTGGCCTCT	ACTTTGTCTA	CTCCAGGTC	GTCTTCTCCG	GGGAAGGCTG	4920
CTTCCCCAAG	GCCACCCCCA	CCCCTCTCTA	CCTGGCCAC	GAGGTCCAGC	TCTTCTCCTC	4980
CCAGTACCCC	TTCCACGTGC	CGCTCCTCAG	CGCTCAGAAG	TCCGTGTGCC	CCGGGCCACA	5040
GGGACCTTGG	GTGCGCTCTG	TGTACCAGGG	GGCTGTGTTT	CTGCTCACCC	AGGGAGATCA	5100
GCTGTCCACA	CACACAGACG	GCACCCCCCA	CCTGCTCCTC	AGCCCCAGTA	GCGTCTTCTT	5160
TGGAGCCTTC	GCTCTATAGA	AGAATCCAGA	AAGAAAAAAA	TTGGTTTCAA	GGCCTTCTCC	5220
CCTTTTCACC	TCCCTTATGA	CCACTTCGGA	GGTCACCGCG	CCTCTCCTCT	GACAATTTCC	5280
AACAGTCTCA	TCTTCCCCCA	CGCTCAGCAC	CTGGAGCTTC	TGTAGAAGGA	ATTCTAGGCA	5340
CCTCGGGGGA	ACTGGAACCA	CCCCGGATGC	TCTGCTGAGG	ATCTGAATGC	CCGCCTGGAG	5400
CCCTTCCCCCT	GTCTTGCCCC	TCTAGGGGCC	CTCGTCCAGG	ACGTGGAAGG	GAAGCTGACC	5460
CATGAGGGAC	TTTGAACGGA	TGACCGGAGC	GGTGTGGGGG	GTTATTTAT	GAAGGGGAAA	5520
ATTAAATTAT	TTATTTATGG	AGGATGGAGA	GAAGGGAATC	ACAGAGGGAT	GTCAGAAGAG	5580
TGTGACACAT	GTGCCCAAGA	GATAAAGTGA	CAGAAGGCAT	GGGCTCCAGA	TGACCCGGCC	5640
AGAGAGGGCA	AAGTGGCTCA	GGAAGGGGCT	GCTTGACTGG	AGGCTCATGA	GGAGACGGCT	5700
GACCCTCGAT	GAAACCCAAT	AAAGCTCTTT	TCTCTGAAAT	GCTGTCTGCT	CGTATCTGTC	5760
ACTCGGGAGG	GGAGAATTCT	CCAGATGTCT	CTAAGGAGTG	GAGGGAGGAC	AGGAATCAGA	5820
GGGGACGGGA	GCTGTGGGTG	TGTGATGAGG	CCTAAGGGGC	TCAGGTGAGA	GATGGCGGCC	5880
TCAGGGTGAG	GGCAGCCAGA	CCCCTGACAG	AGAAGCAGAT	GGTTCCTCTG	AGAAGACAAA	5940
GGAAGAGATG	CAGGGCCAAG	GTCTTGAGAA	CCGAGGTCGG	GGGTCGCCTG	GCAGATATGG	6000
CCACAGGTAG	AGGGACAGAG	GAATAGGGGT	GACAGGAGGC	TTCCCGGGAG	AAGGGAACAC	6060
ACTGAGGGGT	GTTCCGGATT	CTGAGGGAGG	AGCACGGGGA	CGCCCTGGGA	GACATGCCGT	6120
CCAGGGCCAT	GAGGAGTGGG	AGAGCCTCTG	AGGCTAGCGG	CTGGAGATAC	AGGGACATTT	6180
GAGGAGACAC	GGTCATGGCC	AGGAGCCGCG	AGGGCCTGGA	CAGTCTCTAG	GAATCTCGAA	6240
GAAGCAGGAA	TTCTTTGAGG	ATACGTGGCC	ACACAAAGGG	AGGCTGAGGT	GTGGGGACTT	6300
CATGCAGAAG	TCAGGGCCTC	ACATTCCTTT	GGAAGCCGAG	ACTGAAACCA	GCAGCAGAGT	6360
TTTGGTGAGT	TCCTGTGAGA	GTGAAAGGAG	AAGGCCCGCC	ATGGTGGGTT	TGTGAATTCC	6420
CAGCCTGGCT	TCCTCTCCCT	CTGGGGCTGT	CCCAGGCCCT	TTCTTGCCGT	CCTCCCCCAG	6480
CCCGTGTAGG	GCCTCCAGCT	GCCCTTCTCC	CAGCTCCTCT	TCCCTCCAGG	AGACGAAACA	6540
TGGGTCTCAG	CACCCAGCGC	GGTGTCTGCT	AAGTTTTCTC	TCCATTAAAG	ACTCAGCTTT	6600
CTGAAGCTCC	TCCCATTCTC	AGTTCTACCC	CTACCTGAGC	CCTGTTCCGA	AATCAGAGAG	6660

AAATAGAAGT	CATCCCCCAA	AGAAAAGGAA	TTTGTCCCCC	AAAGAAACAG	AACTTGTCCC	6720
CCAAAGAAAT	GGAAACAATG	GGAAATGGGA	GGCAGGGGGG	ACCTGGGGTC	CAGCCTCCAG	6780
GGTCCTACAC	ACAGAGCAGT	AACTGGCCCA	GCAAGCCAC	CTCAGGATCC	GGGCAGGGAG	6840
GGTAGGAAGT	ATCCCTGATG	CCTGGGTGTC	CCCAACTTTC	CAAACCGCCG	CCCCCGCTAT	6900
GGAGATGAAA	CTAAGACAGA	AGGTGCAGGG	CCCGCTACCG	CTTCCTCCAG	ATGAGCTCAT	6960
GGGTTTCTCC	ACCAAGGAAG	TTTTCCGCTG	GTTGAAAGAG	AGCCTCTCCC	CGCCCTCTTC	7020
TCACCCAGAG	CGTATAAATG	CAGCTGTTTG	CACACCCAGC	CAGCAGAAGC	TCCCAGAGTG	7080
AGGACACCAG	GGGACCAGCC	AGGAGAGAGA	CAAGCCATCT	CCAGGACCCC	CTAGAAATAA	7140
CCTCTCAGAA	GACACACCCC	CGAACAGGCA	GCCGGACGAC	TCTCTCCCTC	TCACACGCTG	7200
CCCCGGGGCG	CCACCATCTC	CCAGCTGGAC	CTGAGCCCCT	CTGAAAAAGA	CACCATGAGC	7260
ACTGAGAGCA	TGATCCGAGA	CGTGGAGCTG	GCGGAGGAGG	CGCTCGCCAA	GAAGGCCGGG	7320
GGCCCCCAGG	GCTCCAGGAG	GTGCCTGTGC	CTCAGCCTCT	TCTCCTTCCT	CCTGGTCGCA	7380
GGAGCCACCA	CGCTCTTCTG	CCTACTGCAC	TTTCGAGGTTA	TCGGCCCCCA	GAAGGAAGAG	7440
GTGAGCGCCT	GGCCAGCCTT	GGCTCATTCT	CCCACCCGGA	GAGAAATGGG	GAAGAAAGAG	7500
GGCCAGAGAC	GAGCTGGGGG	AAAGAAGTGT	GCTGATGGGG	AGTGTGGGGA	GGAAATCATG	7560
GAGAAAGATG	GGGAGGCAGA	AGGAGACGTG	GAGAGAGATG	GGGGGAGAGA	GAGAAGGATG	7620
GAGAGAAATC	CGGTGGCCCC	GCCCTTGGA	ATGCTCTCTA	AATATTTGTT	GCACGAATGA	7680
GTGAGTAAGC	AGGGACACCG	ATATAAAGAG	AGATGAGTAG	ACAGACAAGG	GGTGTGGTAG	7740
AAAGATAGGG	AAAAAACAA	TGATCTGGAT	AAAGATAGTG	AGACAGGAAG	AGGTAGAGGA	7800
GATAGGAAAG	AGAGATAAGG	AGAGAAGAAG	GAAGCGTGGG	TGTCTGGCAC	GTGGAAGGCA	7860
CTCAATGAAG	GAGTTGTTGA	ATGGATGGGT	GGATGAGAAA	ATGGATGAGT	GGAGAGAAAA	7920
AACTAGACAT	CAGGGCAGAG	AGTACAAGCT	AGAGAAGCAG	GTGGCTGTTT	TCCCTTCAGA	7980
GGGGACTTAT	TCAAACTAA	TTAATCCTTC	TTCTTCTCCC	CAACAGTTTC	CAGCTGGCCC	8040
CTTGAGCATC	AACCCTCTGG	CCCAAGGACT	CAGTAAGTAT	CTCTAAAAACC	TGTCTCTCAG	8100
TTCTGAGCTT	GGACAGGGGT	GGGGTTAGTG	CTGGGGTGGA	AGGAAGAAGG	GAAATTTAGG	8160
GTCTGGGTTT	GGCGGGGGGA	ATGCAGGTCA	AAGTAGTGAG	ATATTTTCTG	GGAAGTCTGA	8220
GGGTCTCATC	TTTTTCTTTC	CTCTTTCCTC	CTCAGGATCA	TCGTCTCAAA	CCTCAGATAA	8280
GCCCCGTCGCC	CACGTTGTAG	GTAAGAGTTC	TGAGGATGTG	TCTGGGGGAT	GAAGAAATAG	8340
GCAGGACAGA	GAGGGATAGG	ATTTGGGGGC	TGAAGCCAGG	CTGAGGGTAG	CCAGAGCTTG	8400
GAGATAGTAT	GAGGAGGACT	CGCTGAGCTC	CAGGGGAGGA	TGGGGGATAC	TCAGAACTTG	8460
AGGAGGATAC	TCGGAACCTC	ATGGACAGAT	GGGATGTGGG	AAGACAGACC	GAGGGGACAG	8520
GAACCGGATG	TGGGGGGCGG	GCAGAACTCG	AGGGCCAGGA	TGTGGAGAGT	GGAACGTGACA	8580
GGGTACACT	GACTCACCCC	TCCCTCTTTG	TCTCCTCCCT	CCAGCCAATG	TCAAAGCCGA	8640
GGGACAGCTC	CAATGGCAGA	GTGGGTATGC	CAATGCCCTC	CTGGCCAACG	GCGTGAAGCT	8700
GAAAGACAAC	CAGCTGGTGG	TGCCGACAGA	TGGGTGTATC	CTCATCTACT	CCCAGGTCCT	8760
CTTCAGGGGC	CAAGGCTGCC	CTTCCACCAA	CGTTTTCTCT	ACTCACACCA	TCAGCCGCAT	8820
CGCCGTCTCC	TACCAGACCA	AGGTCAACCT	CCTCTCTGCC	ATCAAGAGCC	CTTGCCAGAG	8880
GGAGACCCCC	GAGGGGGCCG	AGGCCAAGCC	CTGGTACGAA	CCCATCTACC	TGGGAGGGGT	8940
CTTCCAGCTG	GAGAAGGATG	ATCGACTCAG	TGCCGAGATC	AACCTGCCCC	ACTATCTGGA	9000
CTTTGCTGAA	TCTGGGCAGG	TCTATTTTGG	GATCATTGCC	CTGTGAGGGG	GCAGGACATC	9060
CGTTCCCTCC	CCTGTCCATC	CCTTTATTAT	TTTACTCCTT	CAGACCCCTT	CACGTCCTTC	9120
TGGTTTtagaa	AGAGAATGAG	GGGCTGGGGA	CTGGGCTCCA	AGCTTAAAC	TTTAAACAAC	9180
AACAGCAACA	CTTAGAAATC	AGGGATTGAG	GGATGTGTGG	CCTGGACAAC	CAGGCACCTGA	9240
CCACCACCAA	GAATTGGAAC	TGGGGCTTCC	AGACTCGCTG	GGGTCTTGG	GTTTGGATTTC	9300
CTGGATGCAA	CCTGGGACAT	CTGGAATGTG	GCTGCCAGGG	AAGCTTGGGT	TCCAATCGGA	9360
ATACTTCAGA	ACATTCCCTG	AGAAGATTTT	ACCTCAATCT	TGATGACTTT	TTAGGCTTCC	9420
CTTTCTTCCA	ATTTTCCAGA	CTTCCCTGGG	ATGGGGAGCC	CAGCCCCAAA	CCCCACAGGC	9480
CAGCTCCCTC	TTATTTATAT	TTGCACTTGG	CATTATTATT	TATTTATTTA	TTTATTATTT	9540
ATTTACTAGT	GAATGTATTT	ATTCAGGAGG	GCGAGGTGTC	CTGGGAGACC	CAGCATAAGG	9600

GCTGCCTTGG	TTCAGATGTG	TTTTCTGTGA	AAACGGAGCT	GAAGTGTAGG	TTGCTCCAC	9660
CTGGCCTCCT	AGCCTCTGTG	CCTCCTTTTG	CTTATGTTTT	TAAAAACAAA	TATTTATCTG	9720
ATCGAGTTGT	CTAAATAATG	CTGATTTGGT	GACTAACTTG	TCGCTACATC	GCTGAACCTC	9780
TGCTCCCCAG	GGGAGTTGTG	TCTGTAACCG	CCCTACTGGT	CAGTGGCGAG	AAATAAAAGC	9840
GTGCTTAGAA	AAGAAATCTG	GCCTCTTTCT	GCGACTGAAT	TCTGCATCTC	CTTGGGGGGG	9900
TGAGGCTGCT	CCCCAAAATT	CTTTCTCCAC	CGGGCTTAGG	ATTCCCTGGG	CTTCACTCCT	9960
GAGCTTGGAC	TGCCTGGCTC	AGGAGCCTCT	GCAAGAAACA	AAGCCCAGCC	AAACAGGTCC	10020
CTCCCCTAAG	AAAGGAACCT	GAAGGTAATT	ACCTCTCCCT	CAGGGTGTGG	GAATTTCCAA	10080
GTCTGGGAAT	TCCTATCCAG	CTGGGGAAGT	CTGCAGTGCA	GGTGAGACTT	CCGGCTGAAA	10140
GAGCCAGGGA	GCGGCCAGAT	GCTCAGGTAC	CTGAACCAGA	GCCAAGGGAC	TTCCAGACAG	10200
TGAGGCAACT	GGGCTCCAAA	TAACCTGATC	CGGGGAATTC			10240

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1644 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CCTCAGCGAG	GACAGCAAGG	GACTAGCCAG	GAGGGAGAAC	AGAAACTCCA	GAACATCCTG	60
GAAATAGCTC	CCAGAAAAGC	AAGCAGCCAA	CCAGGCAGGT	TCTGTCCCTT	TCACTCACTG	120
GCCCCAAGCG	CCACATCTCC	CTCCAGAAAA	GACACCATGA	GCACAGAAAG	CATGATCCGC	180
GACGTGGAAC	TGGCAGAAGA	GGCACTCCCC	CAAAAGATGG	GGGGCTTCCA	GAAGTCCAGG	240
CGGTGCCCTAT	GTCTCAGCCT	CTTCTCATT	CTGCTTGTGG	CAGGGGCCAC	CACGCTCTTC	300
TGTCTACTGA	ACTTCGGGGT	GATCGGTCCC	CAAAGGGATG	AGAAGTTCCC	AAATGGCCTC	360
CCTCTCATCA	GTTCTATGGC	CCAGACCCTC	ACACTCAGAT	CATCTTCTCA	AAATTCGAGT	420
GACAAGCCTG	TAGCCCACGT	CGTAGCAAAC	CACCAAGTGG	AGGAGCAGCT	GGAGTGGCTG	480
AGCCAGCGCG	CCAACGCCCT	CCTGGCCAAC	GGCATGGATC	TCAAAGACAA	CCAAGTAGTG	540
GTGCCAGCCG	ATGGGTTGTA	CCTTGTCTAC	TCCCAGGTTT	TCTTCAAGGG	ACAAGGCTGC	600
CCCGACTACG	TGCTCCTCAC	CCACACCGTC	AGCCGATTTG	CTATCTCATA	CCAGGAGAAA	660
GTCAAACCTC	TCTCTGCCGT	CAAGAGCCCC	TGCCCCAAGG	ACACCCCTGA	GGGGGCTGAG	720
CTCAAACCTC	GGTATGAGCC	CATATACCTG	GGAGGAGTCT	TCCAGCTGGA	GAAGGGGGAC	780
CAACTCAGCG	CTGAGGTCAA	TCTGCCCAAG	TACTTAGACT	TTGCGGAGTC	CGGGCAGGTC	840
TACTTTGGAG	TCATTGCTCT	GTGAAGGGAA	TGGGTGTTCA	TCCATTCTCT	ACCCAGCCCC	900
CACCTCTGACC	CCTTTACTCT	GACCCCTTTA	TTGTCTACTC	CTCAGAGCCC	CCAGTCTGTG	960
TCCTTCTAAC	TTAGAAAGGG	GATTATGGCT	CAGAGTCCAA	CTCTGTGCTC	AGAGCTTTCA	1020
ACAAGTACTC	AGAAACACAA	GATGCTGGGA	CAGTGACCTG	GACTGTGGGC	CTCTCATGCA	1080
CCACCATCAA	GGACTCAAAT	GGGCTTTCCG	AATTCAGTGG	AGCCTCGAAT	GTCCATTCCCT	1140
GAGTTCTGCA	AAGGGAGAGT	GGTCAGGTTG	CCTCTGTCTC	AGAATGAGGC	TGGATAAGAT	1200
CTCAGGCCTT	CCTACCTTCA	GACCTTTCCA	GACTCTTCCC	TGAGGTGCAA	TGCACAGCCT	1260
TCCTCACAGA	GCCAGCCCCC	CTCTATTTAT	ATTTGCACTT	ATTATTTATT	ATTTATTTAT	1320
TATTTATTTA	TTTGCTTATG	AATGTATTTA	TTTGGAAGGC	CGGGGTGTCC	TGGAGGACCC	1380
AGTGTGGGAA	GCTGTCTTCA	GACAGACATG	TTTTCTGTGA	AAACGGAGCT	GAGCTGTCCC	1440

CACCTGGCCT	CTCTACCTTG	TTGCCTCCTC	TTTTGCTTAT	GTTTAAAACA	AAATATTTAT	1500
CTAACCCAAT	TGTCTTAATA	ACGCTGATTT	GGTGACCAGG	CTGTCGCTAC	ATCACTGAAC	1560
CTCTGCTCCC	CACGGGAGCC	GTGACTGTAA	TTGCCCTACA	GTCAATTGAG	AGAAATAAAG	1620
ATCGCTTAAA	ATAAAAAACC	CCCC				1644

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	1890 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single
(D)	TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

AAACAGAGAG	AGATAGAGAA	AGAGAAAGAC	AGAGGTGTTT	CCCTTAGCTA	TGGAAACTCT	60
ATAAGAGAGA	TCCAGCTTGC	CTCCTCTTGA	GCAGTCAGCA	ACAGGGTCCC	GTCCTTGACA	120
CCTCAGCCTC	TACAGGACTG	AGAAGAAGTA	AAACCGTTTG	CTGGGGCTGG	CCTGACTCAC	180
CAGCTGCCAT	GCAGCAGCCC	TTCAATTACC	CATATCCCCA	GATCTACTGG	GTGGACAGCA	240
GTGCCAGCTC	TCCCTGGGCC	CCTCCAGGCA	CAGTTCTTCC	CTGTCCAACC	TCTGTGCCCC	300
GAAGGCCTGG	TCAAAGGAGG	CCACCACCAC	CACCGCCACC	GCCACCACCTA	CCACCTCCGC	360
CGCCGCCGCC	ACCACTGCCT	CCACTACCGC	TGCCACCCCT	GAAGAAGAGA	GGAACCACA	420
GCACAGGCCT	GTGTCTCCTT	GTGATGTTTT	TCATGGTTCT	GTTGCCTTG	GTAGGATTGG	480
GCCTGGGGAT	GTTTCAGCTC	TTCCACCTAC	AGAAGGAGCT	GGCAGAACTC	CGAGAGTCTA	540
CCAGCCAGAT	GCACACAGCA	TCATCTTTGG	AGAAGCAAAT	AGGCCACCCC	AGTCCACCCC	600
CTGAAAAAAA	GGAGCTGAGG	AAAGTGGCCC	ATTTAACAGG	CAAGTCCAAC	TCAAGGTCCA	660
TGCCCTCTGA	ATGGGAAGAC	ACCTATGGAA	TTGTCCTGCT	TTCTGGAGTG	AAGTATAAGA	720
AGGGTGGCCT	TGTGATCAAT	GAAACTGGGC	TGTACTTTGT	ATATTCCAAA	GTATACTTCC	780
GGGGTCAATC	TTGCAACAAC	CTGCCCCTGA	GCCACAAGGT	CTACATGAGG	AACCTCTAAGT	840
ATCCCCAGGA	TCTGGTGATG	ATGGAGGGGA	AGATGATGAG	CTACTGCACT	ACTGGGCAGA	900
TGTGGGCCCC	CAGCAGCTAC	CTGGGGGCAG	TGTTCAATCT	TACCAGTGCT	GATCATTTAT	960
ATGTCAACGT	ATCTGAGCTC	TCTCTGGTCA	ATTTTGAGGA	ATCTCAGACG	TTTTTCGGCT	1020
TATATAAGCT	CTAAGAGAAG	CACTTTGGGA	TTCTTTCCAT	TATGATTCTT	TGTTACAGGC	1080
ACCGAGAATG	TTGTATTTCAG	TGAGGGTCTT	CTTACATGCA	TTTGAGGTCA	AGTAAGAAGA	1140
CATGAACCAA	GTGGACCTTG	AGACCACAGG	GTTCAAAATG	TCTGTAGCTC	CTCAACTCAC	1200
CTAATGTTTA	TGAGCCAGAC	AAATGGAGGA	ATATGACGGA	AGAACATAGA	ACTCTGGGCT	1260
GCCATGTGAA	GAGGGAGAAG	CATGAAAAAG	CAGCTACCCA	GGTGTTCCTAC	ACTCATCTTA	1320
GTGCCTGAGA	GTATTTAGGC	AGATTGAAAA	GGACACCTTT	TAACCTCACCT	CTCAAGGTGG	1380
GCCTTGCTAC	CTCAAGGGGG	ACTGTCCTTC	AGATACATGG	TTGTGACCTG	AGGATTTAAG	1440
GGATGGAAAA	GGAAGACTAG	AGGCTTGCAT	AATAAGCTAA	AGAGGCTGAA	AGAGGCCAAT	1500
GCCCCACTGG	CAGCATCTTC	ACTTCTAAAT	GCATATCCTG	AGCCATCGGT	GAAACTAACA	1560
GATAAGCAAG	AGAGATGTTT	TGGGGACTCA	TTTCATTCCCT	AACACAGCAT	GTGTATTTCC	1620
AGTGCCAATT	GTAGGGGTGT	GTGTGTGTGT	GTGTGTGTGT	GTGTATGACT	AAAGAGAGAA	1680
TGTAGATATT	GTGAAGTACA	TATTAGGAAA	ATATGGGTTG	CATTTGGTCA	AGATTTTGAA	1740
TGCTTCCTGA	CAATCAACTC	TAATAGTGCT	TAAAAATCAT	TGATTGTCAG	CTACTAATGA	1800
TGTTTTCTTA	TAATATAATA	AATATTTATG	TAGATGTGCA	TTTTTGTGAA	ATGAAAACAT	1860
GTAATAAAAA	GTATATGTTA	GGATACAAAT				1890

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1541 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

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GGGTGTCTCA CAGAGAAGCA AAGAGAAGAG AACAGGAGAA ATGGTGTTC CCTTGACTGC      60
GGAAACTTTA TAAAGAAAAC TTAGCTTCTC TGGAGCAGTC AGCGTCAGAG TTCTGTCCTT      120
GACACCTGAG TCTCCTCCAC AAGGCTGTGA GAAGGAAACC CTTTCCTGGG GCTGGGTGCC      180
ATGCAGCAGC CCATGAATTA CCCATGTCCC CAGATCTTCT GGGTAGACAG CAGTGCCACT      240
TCATCTTGGG CTCCTCCAGG GTCAGTTTTT CCCTGTCCAT CTTGTGGGCC TAGAGGGCCG      300
GACCAAAGGA GACCGCCACC TCCACCACCA CCTGTGTCAC CACTACCACC GCCATCACAA      360
CCACTCCCAC TGCCGCCACT GACCCCTCTA AAGAAGAAGG ACCACAACAC AAATCTGTGG      420
CTACCGGTGG TATTTTTCAT GGTCTGGTG GCTCTGGTTG GAATGGGATT AGGAATGTAT      480
CAGCTCTTCC ACCTGCAGAA GGAAGTGGCA GAACTCCGTG AGTTCACCAA CCAAAGCCTT      540
AAAGTATCAT CTTTGTAAAA GCAAATAGCC AACCCTAGTA CACCCTCTGA AAAAAAGAG      600
CCGAGGAGTG TGGCCCATTT AACAGGGAAC CCCCCTCAA GGTCCATCCC TCTGGAATGG      660
GAAGACACAT ATGGAACCGC TCTGATCTCT GGAGTGAAGT ATAAGAAAGG TGGCCTTGTG      720
ATCAACGAAA CTGGGTGTGA CTTCTGTAT TCCAAAGTAT ACTTCCGGGG TCAGTCTTGC      780
AACAACCAGC CCTTAAACCA CAAGGTCTAT ATGAGGAACT CTAAGTATCC TGAGGATCTG      840
GTGCTAATGG AGGAGAAGAG GTTGAAGTAC TGCACTACTG GCCAGATATG GGCCACACAGC      900
AGCTACCTGG GGGCAGTATT CAATCTTACC AGTGCTGACC ATTTATATGT CAACATATCT      960
CAACTCTCTC TGATCAATTT TGAGGAATCT AAGACCTTTT TCGGCTTGTA TAAGCTTTAA      1020
AAGAAAAAGC ATTTTAAAT GATCTACTAT TCTTTATCAT GGGCACCAGG AATATTGTCT      1080
TGAATGAGAG TCTTCTTAAG ACCTATTGAG ATTAATTAAG ACTACATGAG CCACAAAGAC      1140
CTCATGACCG CAAGGTCCAA CAGGTCAGCT ATCCTTCATT TTCTCGAGGT CCATGGAGTG      1200
GTCCTTAATG CCTGCATCAT GAGCCAGATG GAAGGAGGTC TGTGACTGAG GGACATAAAG      1260
CTTTGGGCTG CTGTGTAGCA ATGCAGAGGC ACAGAGAAAG AACTGTCTGA TGTTAAATGG      1320
CCAAGAGAAT TTTAACCATT GAAGAAGACA CCTTTACACT CACTTCCAGG GTGGGTCTAC      1380
TACTACCTC ACAGAGGCCG TTTTGTAGAC ATAGTTGTGG TATGAATATA CAAGGGTGAG      1440
AAAGGAGGCT CATTTGACTG ATAAGCTAGA GACTGAAAAA AAGACAGTGT CTCATTGGCA      1500
CCATCTTTAC TGTTACCTGA TGTTTCTGA GCCGACCTTT G      1541

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(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 888 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GGCTGGTCCC	CTGACAGGTT	GAAGCAAGTA	GACGCCCAGG	AGCCCCGGA	GGGGGCTGCA	60
GTTTCCTTCC	TTCCTTCTCG	GCAGCGCTCC	GCGCCCCCAT	CGCCCCTCCT	GCGCTAGCGG	120
AGGTGATCGC	CGCGGCGATG	CCGGAGGAGG	GTTGCGGCTG	CTCGGTGCGG	CGCAGGCCCT	180
ATGGGTGCGT	CCTGCGGGCT	GCTTTGGTCC	CATTGGTTCG	GGGCTTGGTG	ATCTGCCTCG	240
TGGTGTGCAT	CCAGCGCTTC	GCACAGGCTC	AGCAGCAGCT	GCCGCTCGAG	TCACTTGGGT	300
GGGACGTAGC	TGAGCTGCAG	CTGAATCACA	CAGGACCTCA	GCAGGACCCC	AGGCTATACT	360
GGCAGGGGGG	CCCAGCACTG	GGCCGCTCCT	TCCTGCATGG	ACCAGAGCTG	GACAAGGGGC	420
AGCTACGTAT	CCATCGTGAT	GGCATCTACA	TGGTACACAT	CCAGGTGACG	CTGGCCATCT	480
GCTCCTCCAC	GACGGCCTCC	AGGCACCACC	CCACCACCCT	GGCCGTGGGA	ATCTGCTCTC	540
CCGCCTCCCG	TAGCATCAGC	CTGCTGCGTC	TCAGCTTCCA	CCAAGGTTGT	ACCATTGCCT	600
CCCAGCGCCT	GACGCCCCTG	GCCCCAGGGG	ACACACTCTG	CACCAACCTC	ACTGGGACAC	660
TTTTGCCTTC	CCGAAACACT	GATGAGACCT	TCTTTGGAGT	GCAGTGGGTG	CGCCCCCTGAC	720
CACTGCTGCT	GATTAGGGTT	TTTAAATTT	TATTTTATTT	TATTTAAGTT	CAAGAGAAAA	780
AGTGACACA	CAGGGGCCAC	CCGGGGTTGG	GGTGGGAGTG	TGGTGGGGGG	TAGTGGTGGC	840
AGGACAAGAG	AAGGCATTGA	GCTTTTCTT	TCATTTCTCT	ATTAAAAA		888

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1906 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CCAAGTCACA	TGATTTCAGGA	TTCAGGGGGA	GAATCCTTCT	TGGAACAGAG	ATGGGCCCCAG	60
AACTGAATCA	GATGAAGAGA	GATAAGGTGT	GATGTGGGGA	AGACTATATA	AAGAATGGAC	120
CCAGGGCTGC	AGCAAGCACT	CAACGGAATG	GCCCCCTCTG	GAGACACAGC	CATGCATGTG	180
CCGGCGGGCT	CCGTGGCCAG	CCACCTGGGG	ACCACGAGCC	GCAGCTATTT	CTATTTGACC	240
ACAGCCACTC	TGGTCTCTGT	CCTTGCTCTT	ACGGTGGCCA	CTATTATGGT	GTTGGTCGTT	300
CAGAGGACGG	ACTCCATTCC	CAACTCACCT	GACAACGTCC	CCCTCAAAGG	AGGAAATTGC	360
TCAGAAGACC	TCTTATGTAT	CCTGAAAAGA	GCTCCATTCA	AGAAGTCATG	GGCCTACCTC	420
CAAGTGGCAA	AGCATCTAAA	CAAAACCAAG	TTGTCTTGGA	ACAAAGATGG	CATTCTCCAT	480
GGAGTCAGAT	ATCAGGATGG	GAATCTGGTG	ATCCAATTCC	CTGGTTTGTA	CTTCATCATT	540
TGCCAACTGC	AGTTTCTTGT	ACAATGCCCC	AATAATTCTG	TCGATCTGAA	GTTGGAGCTT	600
CTCATCAACA	AGCATATCAA	AAAACAGGCC	CTGGTGACAG	TGTGTGAGTC	TGGAATGCAA	660
ACGAAACACG	TATACCAGAA	TCTCTCTCAA	TTCTTGCTGG	ATTACCTGCA	GGTCAACACC	720
ACCATATCAG	TCAATGTGGA	TACATTCCAG	TACATAGATA	CAAGCACCTT	TCCTCTTGAG	780
AATGTGTTGT	CCATCTTCTT	ATACAGTAAT	TCAGACTGAA	CAGTTTCTCT	TGGCCTTCAG	840
GAAGAAAGCG	CCTCTCTACC	ATACAGTATT	TCATCCCTCC	AAACACTTGG	GCAAAAAGAA	900
AACTTTAGAC	CAAGACAAAC	TACACAGGGT	ATTAAATAGT	ATACTTCTCC	TTCTGTCTCT	960
TGGAAAGATA	CAGCTCCAGG	GTTAAAAAGA	GAGTTTTTGT	TGAAGTATCT	TTCAGATAGC	1020
AGGCAGGGAA	GCAATGTAGT	GTGGTGGGCA	GAGCCCCACA	CAGAATCAGA	AGGGATGAAT	1080
GGATGTCCCA	GCCCAACCAC	TAATTCAGTG	TATGGTCTTG	ATCTATTTCT	TCTGTTTTGA	1140

GAGCCTCCAG	TTAAAATGGG	GCTTCAGTAC	CAGAGCAGCT	AGCAACTCTG	CCCTAATGGG	1200
AAATGAAGGG	GAGCTGGGTG	TGAGTGTTTA	CACTGTGCCC	TTCACGGGAT	ACTTCTTTTA	1260
TCTGCAGATG	GCCTAATGCT	TAGTTGTCCA	AGTCGCGATC	AAGGACTCTC	TCACACAGGA	1320
AACTTCCCTA	TACTGGCAGA	TACACTTG TG	ACTGAACCAT	GCCCAGTTTA	TGCCTGTCTG	1380
ACTGTCACTC	TGGCACTAGG	AGGCTGATCT	TGTACTCCAT	ATGACCCAC	CCCTAGGAAC	1440
CCCCAGGGAA	AACCAGGCTC	GGACAGCCCC	CTGTTCTCTGA	GATGGAAAGC	ACAAATTTAA	1500
TACACCACCA	CAATGGAAAA	CAAGTTCAAA	GACTTTTACT	TACAGATCCT	GGACAGAAAG	1560
GGCATAATGA	GTCTGAAGGG	CAGTCTCCT	TCTCCAGGTT	ACATGAGGCA	GGAATAAGAA	1620
GTCAGACAGA	GACAGCAAGA	CAGTTAACAA	CGTAGGTAAA	GAAATAGGGT	GTGGTCACTC	1680
TCAATTCACT	GGCAAATGCC	TGAATGGTCT	GTCTGAAGGA	AGCAACAGAG	AAGTGGGGAA	1740
TCCAGTCTGC	TAGGCAGGAA	AGATGCCTCT	AAGTTCCTTG	CTCTGGCCAG	AGGTGTGGTA	1800
TAGAACCAGA	AACCCATATC	AAGGGTGA CT	AAGCCCGGCT	TCCGGTATGA	GAAATTAAAC	1860
TTGTATACAA	AATGGTTGCC	AAGGCAACAT	AAAATTATAA	GAATTC		1906

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1619 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GTCATGGAAT	ACGCCTCTGA	CGCTTCACTG	GACCCCGAAG	CCCCGTGGCC	TCCCGCGCCC	60
CGCGCTCGCG	CCTGCCGCGT	ACTGCCTTGG	GCCCTGGTCG	CGGGGCTGCT	GCTGCTGCTG	120
CTGCTCGCTG	CCGCCGTGCG	CGTCTTCCTC	GCCTGCCCTT	GGGCCGTGTC	CGGGGCTCGC	180
GCCTCGCCCC	GCTCCGCGGC	CAGCCCGAGA	CTCCGCGAGG	GTCCCGAGCT	TTCGCCCCGAC	240
GATCCCGCCG	GCCTCTTGGA	CCTGCGGCAG	GGCATGTTTG	CGCAGCTGGT	GGCCCAAAAT	300
GTTCTGCTGA	TCGATGGGCC	CCTGAGCTGG	TACAGTGACC	CAGGCCTGGC	AGGCGTGTCC	360
CTGACGGGGG	GCCTGAGCTA	CAAAGAGGAC	ACGAAGGAGC	TGGTGGTGGC	CAAGGCTGGA	420
GTCTACTATG	TCTTCTTTCA	ACTAGAGCTG	CGGCGCGTGG	TGGCCGGCGA	GGGCTCAGGC	480
TCCGTTTCAC	TTGCGCTGCA	CCTGCAGCCA	CTGCGCTCTG	CTGCTGGGGC	CGCCGCCCTG	540
GCTTTGACCG	TGGACCTGCC	ACCCGCCCTC	TCCGAGGCTC	GGAACTCGGC	CTTCGGTTTC	600
CAGGGCCGCT	TGCTGCACCT	GAGTGCCGGC	CAGCGCCTGG	GCGTCCATCT	TCACACTGAG	660
GCCAGGGCAC	GCCATGCCTG	GCAGCTTACC	CAGGGCGCCA	CAGTCTTGGG	ACTCTTCCGG	720
GTGACCCCGG	AAATCCCAGC	CGGACTCCCT	TCACCGAGGT	CGGAATAACG	CCCAGCCTGG	780
GTGCAGCCCA	CCTGGACAGA	GTCCGAATCC	TACTCCATCC	TTCATGGAGA	CCCCTGGTGC	840
TGGGTCCCTG	CTGCTTTCTC	TACCTCAAGG	GGCTTGGCAG	GGGTCCCTGC	TGCTGACCTC	900
CCCTTGAGGA	CCCTCCTCAC	CCACTCCTTC	CCCAAGTTGG	ACCTTGATAT	TTATTCTGAG	960
CCTGAGCTCA	GATAATATAT	TATATATATT	ATATATATAT	ATATATTTCT	ATTTAAAGAG	1020
GATCCTGAGT	TTGTGAATGG	ACTTTTTTAG	AGGAGTTGTT	TTGGGGGGGG	GGTCTTCGAC	1080
ATTGCCGAGG	CTGGTCTTGA	ACTCCTGGAC	TTAGACGATC	CTCCTGCCTC	AGCCTCCCAA	1140
GCAACTGGGA	TTCATCCTTT	CTATTAATTC	ATTGTACTTA	TTTGCCTATT	TGTGTGTATT	1200
GAGCATCTGT	AATGTGCCAG	CATTGTGCCC	AGGCTAGGGG	GCTATAGAAA	CATCTAGAAA	1260
TAGACTGAAA	GAAAATCTGA	GTTATGGTAA	TACGTGAGGA	ATTTAAAGAC	TCATCCCCAG	1320
CCTCCACCTC	CTGTGTGATA	CTTGGGGGCT	AGCTTTTTTC	TTTCTTTCTT	TTTTTTTGAGA	1380

TGGTCTTGTT	CTGTCAACCA	GGCTAGAATG	CAGCGGTGCA	ATCATGAGTC	AATGCAGCCT	1440
CCAGCCTCGA	CCTCCCGAGG	CTCAGGTGAT	CCTCCCATCT	CAGCCTCTCG	AGTAGCTGGG	1500
ACCACAGTTG	TGTGCCACCA	CACTTGGCTA	ACTTTTAAAT	TTTTTTGCGG	AGACGGTATT	1560
GCTATGTTGC	CAAGGTTGTT	TACATGCCAG	TACAATTTAT	AATAAACACT	CATTTTTTCC	1619

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	1239 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single
(D)	TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

AGCCTATAAA	GCACGGGCAC	TGGCGGGAGA	CGTGCACTGA	CCGACCGTGG	TAATGGACCA	60
GCACACACTT	GATGTGGAGG	ATACCGCGGA	TGCCAGACAT	CCAGCAGGTA	CTTCGTGCCC	120
CTCGGATGCG	GCGCTCCTCA	GAGATACCGG	GCTCCTCGCG	GACGCTGCGC	TCCTCTCAGA	180
TACTGTGCGC	CCCACAAATG	CCGCGCTCCC	CACGGATGCT	GCCTACCCTG	CGGTTAATGT	240
TCGGGATCGC	GAGGCCGCGT	GGCCGCCTGC	ACTGAACTTC	TGTTCCCGCC	ACCCAAAGCT	300
CTATGGCCTA	GTCGCTTTGG	TTTGTGCTGCT	TCTGATCGCC	GCCTGTGTTC	CTATCTTCAC	360
CCGCACCGAG	CCTCGGCCAG	CGCTCACAAT	CACCACCTCG	CCCAACCTGG	GTACCCGAGA	420
GAATAATGCA	GACCAGGTCA	CCCCTGTTTC	CCACATTGGC	TGCCCCAACA	CTACACAACA	480
GGGCTCTCCT	GTGTTGCGCA	AGCTACTGGC	TAAAAACCAA	GCATCGTTGT	GCAATACAAC	540
TCTGAACCTG	CACAGCCAAG	ATGGAGCTGG	GAGCTCATA	CTATCTCAAG	GTCTGAGGTA	600
CGAAGAAGAC	AAAAAGGAGT	TGGTGGTAGA	CAGTCCCGGG	CTCTACTACG	TATTTTTGGA	660
ACTGAAGCTC	AGTCCAACAT	TCACAAACAC	AGGCCACAAG	GTGCAGGGCT	GGGTCTCTCT	720
TGTTTTGCAA	GCAAAGCCTC	AGGTAGATGA	CTTTGACAAC	TTGGCCCTGA	CAGTGGAAC	780
GTTCCCTTGC	TCCATGGAGA	ACAAGTTAGT	GGACCGTTCC	TGGAGTCAAC	TGTTGCTCCT	840
GAAGGCTGGC	CACCGCCTCA	GTGTGGGTCT	GAGGGCTTAT	CTGCATGGAG	CCCAGGATGC	900
ATACAGAGAC	TGGGAGCTGT	CTTATCCCAA	CACCACCAGC	TTTGGACTCT	TTCTTGTGAA	960
ACCCGACAAC	CCATGGGAAT	GAGAACTATC	CTTCTTGTGA	CTCCTAGTTG	CTAAGTCCTC	1020
AAGCTGCTAT	GTTTTATGGG	GTCTGAGCAG	GGGTCCCTTC	CATGACTTTC	TCTTGTCTTT	1080
AACTGGACTT	GGTATTTATT	CTGAGCATAG	CTCAGACAAG	ACTTTATATA	ATTCACTAGA	1140
TAGCATTAGT	AAACTGCTGG	GCAGCTGCTA	GATAAAAAAA	AATTTCTAAA	TCAAAGTTTA	1200
TATTTATATT	AATATATAAA	AATAAATGTG	TTTGTAAT			1239

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	606 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single
(D)	TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ATGATCGAAA	CATACAACCA	AACTTCTCCC	CGATCTGCGG	CCACTGGACT	GCCCATCAGC	60
ATGAAAATTT	TTATGTATTT	ACTTACTGTT	TTTCTTATCA	CCCAGATGAT	TGGGTCAGCA	120
CTTTTTGCTG	TGTATCGCTT	CGCACAGGCT	TTTGAAATGC	AAAAAGGTGA	TCAGAATCCT	180
CAAATTGCGG	CACATGTCAT	AAGTGAGGCC	AGCAGTAAAA	CAACATCTGT	GTTACAGTGG	240
GCTGAAAAAG	GATACTACAC	CATGAGCAAC	AACTTGGTAA	CCCTGGAAAA	TGGGAAACAG	300
CTGACCGTTA	AAAGACAAGG	ACTCTATTAT	ATCTATGCCC	AAGTCACCTT	CTGTTCCAAT	360
CGGGAAGCTT	CGAGTCAAGC	TCCATTTATA	GCCAGCCTCT	GCCTAAAGTC	CCCCGGTAGA	420
TTCGAGAGAA	TCTTACTCAG	AGCTGCAAAT	ACCCACAGTT	CCGCCAAACC	TTGCGGGCAA	480
CAATCCATTC	ACTTGGGAGG	AGTATTTGAA	TTGCAACCAG	GTGCTTCGGT	GTTTGTCAAT	540
GTGACTGATC	CAAGCCAAGT	GAGCCATGGC	ACTGGCTTCA	CGTCCTTTGG	CTTACTCAAA	600
CTCTGA						606

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 783 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

ATGATCGAAA	CATACAACCA	AACTTCTCCC	CGATCTGCGG	CCACTGGACT	GCCCATCAGC	60
ATGAAAATTT	TTATGTATTT	ACTTACTGTT	TTTCTTATCA	CCCAGATGAT	TGGGTCAGCA	120
CTTTTTGCTG	TGTATCTTCA	TAGAAGATTG	GATAAGGTCG	AAGAGGAAGT	AAACCTTCAT	180
GAAGATTTTG	TATTCATAAA	AAAGCTAAAG	AGATGCAACA	AAGGAGAAGG	ATCTTTATCC	240
TTGCTGAAC	GTGAGGAGAT	GAGAAGGCAA	TTTGAAGACC	TTGTCAAGGA	TATAACGTTA	300
AACAAAGAAG	AGAAAAAGA	AAACAGCTTT	GAAATGCAAA	AAGGTGATCA	GAATCCTCAA	360
ATTGCGGCAC	ATGTCATAAG	TGAGGCCAGC	AGTAAAACAA	CATCTGTGTT	ACAGTGGGCT	420
GAAAAAGGAT	ACTACACCAT	GAGCAACAAC	TTGGTAACCC	TGGAAAATGG	GAAACAGCTG	480
ACCGTTAAAA	GACAAGGACT	CTATTATATC	TATGCCCAAG	TCACCTTCTG	TTCCAATCGG	540
GAAGCTTCGA	GTCAAGCTCC	ATTTATAGCC	AGCCTCTGCC	TAAAGTCCCC	CGGTAGATTG	600
GAGAGAATCT	TACTCAGAGC	TGCAAATACC	CACAGTTCCG	CCAAACCTTG	CGGGCAACAA	660
TCCATTCACT	TGGGAGGAGT	ATTTGAATTG	CAACCAGGTG	CTTCGGTGTT	TGTCAATGTG	720
ACTGATCCAA	GCCAAGTGAG	CCATGGCACT	GGCTTCACGT	CCTTTGGCTT	ACTCAAACCTC	780
TGA						783

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 558 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

CTGCTGCACT	TCGGGGTAAT	CGGCCCCCAG	AGGGAAGAGC	AGTCCCCAGG	TGGCCCCCTCC	60
ATCAACAGCC	CTCTGGTTCA	AACACTCAGG	TCCTCTTCTC	AAGCCTCAAG	TAACAAGCCG	120
GTAGCCACG	TTGTAGCCGA	CATCAACTCT	CCGGGGCAGC	TCCGGTGGTG	GGACTCGTAT	180
GCCAATGCCC	TCATGGCCAA	CGGTGTGAAG	CTGGAAGACA	ACCAGCTGGT	GGTGCCTGCT	240
GACGGGCTTT	ACCTCATCTA	CTCACAGGTC	CTCTTCAGGG	GCCAAGGCTG	CCCTTCCACC	300
CCCTTGTTCC	TCACCCACAC	CATCAGCCGC	ATTGCAGTCT	CCTACCAGAC	CAAGGTCAAC	360
ATCCTGTCTG	CCATCAAGAG	CCCTTGCCAC	AGGGAGACCC	CAGAGTGGGC	TGAGGCCAAG	420
CCCTGGTACG	AACCCATCTA	CCAGGGAGGA	GTCTTCCAGC	TGGAGAAGGG	AGATCGCCTC	480
AGTGCTGAGA	TCAACCTGCC	GGACTACCTG	GACTATGCCG	AGTCCGGGCA	GGTCTACTTT	540
GGGATCATTG	CCCTGTGA					558

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	1783 base pairs
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CAAGTCACAT	GATCCAGGAT	GCAGGGGAAA	ATCCTTCTTG	GAACAGAGCT	GGGTACAGAA	60
CCGAATCAGA	TGAGGAGAGA	TAAGGTGTGA	TGTGGGACAG	ACTATATAAA	GCATGGAGCC	120
AGGGCTGCAA	CAAGCAGGCA	GCTGTGGGGC	TCCTTCCCCT	GACCCAGCCA	TGCAGGTGCA	180
GCCCCGCTCG	GTAGCCAGCC	CCTGGAGAAG	CACGAGGCC	TGGAGAAGCA	CAAGTCGCAG	240
CTACTTCTAC	CTCAGCACCA	CCGCACTGGT	GTGCCTTGTT	GTGGCAGTGG	CGATCATTTCT	300
GGTACTGGTA	GTCCAGAAAA	AGGACTCCAC	TCCAAATACA	ACTGAGAAGG	CCCCCCTTAA	360
AGGAGGAAAT	TGCTCAGAGG	ATCTCTTCTG	TACCTTGAAA	AGTACTCCAT	CCAAGAAGTC	420
ATGGGCCTAC	CTCCAAGTGT	CAAAGCATCT	CAACAATACC	AAACTGTCAT	GGAACGAAGA	480
TGGCACCATC	CACGGACTCA	TATACCAGGA	CGGGAACCTG	ATAGTCCAAT	TCCCTGGCTT	540
GTACTTCATC	GTTTGCCAAC	TGCAGTTCCT	CGTGCAGTGC	TCAAATCATT	CTGTGGACCT	600
GACATTGCAG	CTCCTCATCA	ATTCCAAGAT	CAAAAAGCAG	ACGTTGGTAA	CAGTGTGTGA	660
GTCTGGAGTT	CAGAGTAAGA	ACATCTACCA	GAATCTCTCT	CAGTTTTTGC	TGCATTACTT	720
ACAGGTCAAC	TCTACCATAT	CAGTCAGGGT	GGATAATTTT	CAGTATGTGG	ATACAAACAC	780
TTTCCCTCTT	GATAATGTGC	TATCCGTCTT	CTTATATAGT	AGCTCAGACT	GAATAGTTGT	840
TCTTAACCTT	TATGAAAATG	CTGTCTACCA	TACAGTACTT	CATCTGTCCA	AACATGGGCC	900
AAAGAAAATA	TTAGGACAAC	TCAAATAAG	CATGTGAGTT	AGTGCCTTC	TCTTTCTGTC	960
CTTTGGAAAA	ATACAAACCC	AGGATTTAGA	AAGTGGAGTC	TCCTTCAGAT	GCACAAACAG	1020
GAAAGAATGT	GATATGTGCA	CAGAGACCTA	CTTGGGCACT	AGAAGGGGTG	TGAGTTGTCC	1080
CAGTATAACC	ACTAATTCAC	TGACCTTGAG	CCATTTTTCC	TTCCCCCTGG	AACCTGGGGT	1140
CTGAATCTGG	AAAAGTAGGA	GATGAGATTT	ACATTTCCCC	AATATTTTCT	TCAACTCAGA	1200
AGACGAGACT	GTGGAGCTGA	GCTCCCTACA	CAGATGAAGG	CCTCCCATGG	CATGAGGAAA	1260

ATGATGGTAC	CAGTAATGTC	TGTCTGACTG	TCATCTCAGC	AAGTCCTAAG	GACTTCCATG	1320
CTGCCTTGTT	GAAAGATACT	CTAACCTCTT	GTAATGGGCA	AAGTGATCCT	GTCTCTCACT	1380
GAGGGGAGTA	GCTGCTGCCA	TCTCCTGAGA	CATACATGGA	GACATTTTCT	GCCCAAATTC	1440
CATTCTGTGT	GCAGTTTTTA	AGTATTCCCC	CAAAAGTTCT	TGACAATGAG	AACTTTGAAT	1500
GTGGGAAGAG	CTTCTGGACA	GCAAACATTA	ACAGCTTCTC	CTGACCAGAG	AGACCATGCA	1560
AGCTTGGTCT	TAGACCCATC	AAGCTTGAGG	TTTCTACATT	GTGGGAGACA	GACTTTTGAC	1620
AAACCATTTG	AGTTGATGTC	TGGGCCCCCTG	GGAGTTCTCC	TTCAGTAAGG	AGAGCAAGCC	1680
GTTCTAGTGC	TGTGTCAGAG	GATGGAGTAA	AATAGACACT	TTTCTGAAGG	AAAGGAGAAC	1740
AAAGTTCCAG	AAAAAGGCTA	GAAAATGTTT	AAAAAGAAAA	AAA		1783

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	1047 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single
(D)	TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

AGAGAGCGCT	GGGAGCCGGA	GGGGAGCGCA	GCGAGTTTTG	GCCAGTGGTC	GTGCAGTCCA	60
AGGGGCTGGA	TGGCATGCTG	GACCCAAGCT	CAGCTCAGCG	TCCGGACCCA	ATAACAGTTT	120
TACCAAGGGA	GCAGCTTTCT	ATCCTGGCCA	CACTGAGGTG	CATAGCGTAA	TGTCCATGTT	180
GTTCTACACT	CTGATCACAG	CTTTTCTGAT	CGGCATACAG	GCGGAACCAC	ACTCAGAGAG	240
CAATGTCCCT	GCAGGACACA	CCATCCCCCA	AGTCCACTGG	ACTAAACTTC	AGCATTTCCCT	300
TGACACTGCC	CTTCGCAGAG	CCCGCAGCGC	CCCGGCAGCG	GCGATAGCTG	CACGCGTGGC	360
GGGGCAGACC	CGCAACATTA	CTGTGGACCC	CAGGCTGTTT	AAAAAGCGGC	GACTCCGTTT	420
ACCCCGTGTG	CTGTTTAGCA	CCCAGCCTCC	CCGTGAAGCT	GCAGACACTC	AGGATCTGGA	480
CTTCGAGGTC	GGTGGTGCTG	CCCCCTTCAA	CAGGACTCAC	AGGAGCAAGC	GGTCATCATC	540
CCATCCCATC	TTCCACAGGG	GCGAATTCTC	GGTGTGTGAC	AGTGTGAGCG	TGTGGGTTGG	600
GGATAAGACC	ACCGCCACAG	ACATCAAGGG	CAAGGAGGTG	ATGGTGTGTT	GAGAGGTGAA	660
CATTAACAAC	AGTGTATTCA	AACAGTACTT	TTTTGAGACC	AAGTGCCGGG	ACCCAAATCC	720
CGTTGACAGC	GGGTGCCGGG	GCATTGACTC	AAAGCACTGG	AACTCATATT	GTACCACGAC	780
TCACACCTTT	GTCAAGGCGC	TGACCATGGA	TGGCAAGCAG	GCTGCCTGGC	GGTTTATCCG	840
GATAGATACG	GCCTGTGTGT	GTGTGCTCAG	CAGGAAGGCT	GTGAGAAGAG	CCTGACCTGC	900
CGACACGCTC	CCTCCCCCTG	CCCCTTCTAC	ACTCTCCTGG	GCCCCCTCCT	ACCTCAACCT	960
GTAAATTATT	TTAAATTATA	AGGACTGCAT	GGTAATTTAT	AGTTTATACA	GTTTTAAAGA	1020
ATCATTATTT	ATTAAATTTT	TGGAAGC				1047

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	1176 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

GAGCGCCTGG	AGCCGGAGGG	GAGCGCATCG	AGTGACTTTG	GAGCTGGCCT	TATATTTGGA	60
TCTCCCGGGC	AGCTTTTTTG	AAACTCCTAG	TGAACATGCT	GTGCCTCAAG	CCAGTGAAAT	120
TAGGCTCCCT	GGAGGTGGGA	CACGGGCAGC	ATGGTGGAGT	TTTGGCCTGT	GGTCGTGCAG	180
TCCAGGGGGC	TGGATGGCAT	GCTGGACCCA	AGCTCACCTC	AGTGTCTGGG	CCCAATAAAG	240
GTTTTGCCAA	GGACGCAGCT	TTCTATACTG	GCCGCAGTGA	GGTGCATAGC	GTAATGTCCA	300
TGTTGTTCTA	CACTCTGATC	ACTGCGTTTT	TGATCGGCGT	ACAGGCAGAA	CCGTACACAG	360
ATAGCAATGT	CCCAGAAGGA	GACTCTGTCC	CTGAAGCCCA	CTGGACTAAA	CTTCAGCATT	420
CCCTTGACAC	AGCCCTCCGC	AGAGCCCGCA	GTGCCCCCTAC	TGCACCAATA	GCTGCCCCGAG	480
TGACAGGGCA	GACCCGCAAC	ATCACTGTAG	ACCCACAGACT	GTTTAAGAAA	CGGAGACTCC	540
ACTCACCCCG	TGTGCTGTTT	AGCACCCAGC	CTCCACCCAC	CTCTTCAGAC	ACTCTGGATC	600
TAGACTTCCA	GGCCCATGGT	ACAATCCCTT	TCAACAGGAC	TCACCGGAGC	AAGCGCTCAT	660
CCACCCACCC	AGTCTTCCAC	ATGGGGGAGT	TCTCAGTGTG	TGACAGTGTG	AGTGTGTGGG	720
TTGGAGATAA	GACCACAGCC	ACAGACATCA	AGGGCAAGGA	GGTGACAGTG	CTGGCCGAGG	780
TGAACATTAA	CAACAGTGTA	TTCAGACAGT	ACTTTTTTGA	GACCAAGTGC	CGAGCCTCCA	840
ATCCTGTTGA	GAGTGGGTGC	CGGGGCATCG	ACTCCAAACA	CTGGAATCA	TACTGCACCA	900
CGACTCACAC	CTTCGTCAAG	GCGTTGACAA	CAGATGAGAA	GCAGGCTGCC	TGGAGGTTCA	960
TCCGGATAGA	CACAGCCTGT	GTGTGTGTGC	TCAGCAGGAA	GGCTACAAGA	AGAGGCTGAC	1020
TTGCCTGCAG	CCCCCTTCCC	CACCTGCCCC	CTCCACATC	TCTTGGGCCC	CTCCCTACCT	1080
CAGCCTGTAA	ATTATTTTAA	ATTATAAGGA	CTGCATGATA	ATTTATCGTT	TATACAATTT	1140
TAAAGACATT	ATTTATTAAA	TTTTCAAAGC	ATCCTG			1176

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	1623 base pairs
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

TCAGAGTCCT	GTCCTTGACA	CTTCAGTCTC	CACAAGACTG	AGAGGAGGAA	ACCCTTTCCT	60
GGGGCTGGGT	GCCATGCAGC	AGCCCGTGAA	TTACCCATGT	CCCCAGATCT	ACTGGGTAGA	120
CAGCAGTGCC	ACTTCTCCTT	GGGCTCCTCC	AGGGTCAGTT	TTTTCTTGTC	CATCCTCTGG	180
GCCTAGAGGG	CCAGGACAAA	GGAGACCACC	GCCTCCACCA	CCACCTCCAT	CACCACTACC	240
ACCGCCTTCC	CAACCACCCC	CGCTGCCTCC	ACTAAGCCCT	CTAAAGAAGA	AGGACAACAT	300
AGAGCTGTGG	CTACCGGTGA	TATTTTTTCAT	GGTGCTGGTG	GCTCTGGTTG	GAATGGGGTT	360
AGGAATGTAT	CAACTCTTTC	ATCTACAGAA	GGAAGTGGCA	GAAGTCCGTG	AGTTACACAA	420
CCACAGCCTT	AGAGTATCAT	CTTTTGAAAA	GCAAATAGCC	AACCCAGCA	CACCTCTGA	480
AACCAAAAAG	CCAAGGAGTG	TGGCCCACTT	AACAGGGAAC	CCCCGCTCAA	GGTCCATCCC	540
TCTGGAATGG	GAAGACACAT	ATGGAAGTGC	TTTGATCTCT	GGAGTGAAGT	ATAAGAAAGG	600
CGGCCTTGTTG	ATCAATGAGG	CTGGGTTGTA	CTTCGTATAT	TCCAAAGTAT	ACTTCCGGGG	660

TCAGTCTTGC AACAGCCAGC CCCTAAGCCA CAAGGTCTAT ATGAGGAACT TTAAGTATCC 720
 TGGGGATCTG GTGCTAATGG AGGAGAAGAA GTTGAATTAC TGCACTACTG GCCAGATATG 780
 GGCCACAGC AGCTACCTAG GGGCAGTATT TAATCTTACC GTTGCTGACC ATTTATATGT 840
 CAACATATCT CAACTCTCTC TGATCAATTT TGAGGAATCT AAGACCTTTT TTGGCTTATA 900
 TAAGCTTTAA AGGAAAAAGC ATTTTAGAAT GATCTATTAT TCTTTATCAT GGATGCCAGG 960
 AATATTGTCT TCAATGAGAG TCTTCTTAAG ACCAATTGAG CCACAAAGAC CACAAGGTCC 1020
 AACAGGTCAG CTACCCTTCA TTTTCTAGAG GTCCATGGAG TGGTCCTTAA TGCCTGCATC 1080
 ATGAGCCAGA TGGGAAGAAG ACTGTTCTTG AGGAACATAA AGTTTTGGGC TGCTGTGTGG 1140
 CAATGCAGAG GCAAAGAGAA GGAAGTGTCT GATGTTAAAT GGCCAAGAGC ATTTTAGCCA 1200
 TTGAAGAAAA AAAAAACCTT TAAACTCACC TTCCAGGGTG GGTCTACTTG CTACCTCACA 1260
 GGAGGCCGTC TTTTAGACAC ATGGTTGTGG TATGACTATA CAAGGGTGAG AAAGGATGCT 1320
 AGGTTTCATG GATAAGCTAG AGACTGAAAA AAGCCAGTGT CCCATTGGCA TCATCTTTAT 1380
 TTTTAACTGA TGTTTTCTGA GCCCACCTTT GATGCTAACA GAGAAATAAG AGGGGTGTTT 1440
 GAGGCACAAG TCATTCTCTA CATAGCATGT GTACCTCCAG TGCAATGATG TCTGTGTGTG 1500
 TTTTATGTA TGAGAGTAGA GCGATTCTAA AGAGTCACAT GAGTACAACG CGTACATTAC 1560
 GGAGTACATA TTAGAAACGT ATGTGTTACA TTTGATGCTA GAATATCTGA ATGTTTCTTG 1620
 CTA 1623

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

GTTAAGCTTT TCAGTCAGCA TGATAGAA 28

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

GTTTCTAGAT CAGAGTTTGA GTAAGCC 27

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

CCAAGACTAG TTAACACAGC ATGATCGAAA

30

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

CCAATGCGGC CGCACTCAGA ATTCAACCTG

30

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 972 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

TCTAGACTCA	GGACTGAGAA	GAAGTAAAAC	CGTTTGCTGG	GGCTGGCCTG	ACTCACCAGC	60
TGCCATGCAG	CAGCCCTTCA	ATTACCCATA	TCCCCAGATC	TACTGGGTGG	ACAGCAGTGC	120
CAGCTCTCCC	TGGGCCCTC	CAGGCACAGT	TCTTCCCTGT	CCAACCTCTG	TGCCCAGAAG	180
GCCTGGTCAA	AGGAGGCCAC	CACCACCACC	GCCACCGCCA	CCACTACCAC	CTCCGCCGCC	240
GCCGCCACCA	CTGCCTCCAC	TACCGCTGCC	ACCCCTGAAG	AAGAGAGGGA	ACCACAGCAC	300
AGGCCTGTGT	CTCCTTGTGA	TGTTTTTCAT	GGTTCTGGTT	GCCTTGGTAG	GATTGGGCCT	360
GGGGATGTTT	CAGCTCTTCC	ACCTACAGAA	GGAGCTGGCA	GAAGTCCGAG	AGTCTACCAG	420
CCAGATGCAC	ACAGCATCAT	CTTTGGAGAA	GCAAATAGGC	CACCCCAGTC	CACCCCCTGA	480

AAAAAAGGAG	CTGAGGAAAG	TGGCCCATTT	AACAGGCAAG	TCCAACTCAA	GGTCCATGCC	540
TCTGGAATGG	GAAGACACCT	ATGGAATTGT	CCTGCTTTCT	GGAGTGAAGT	ATAAGAAGGG	600
TGGCCTTGTG	ATCAATGAAA	CTGGGCTGTA	CTTTGTATAT	TCCAAAGTAT	ACTTCCGGGG	660
TCAATCTTGC	AACAACCTGC	CCCTGAGCCA	CAAGGTCTAC	ATGAGGAACT	CTAAGTATCC	720
CCAGGATCTG	GTGATGATGG	AGGGGAAGAT	GATGAGCTAC	TGCACTACTG	GGCAGATGTG	780
GGCCCGCAGC	AGCTACCTGG	GGGCAGTGTT	CAATCTTACC	AGTGCTGATC	ATTTATATGT	840
CAACGTATCT	GAGCTCTCTC	TGGTCAATTT	TGAGGAATCT	CAGACGTTTT	TCGGCTTATA	900
TAAGCTCTAA	GAGAAGCACT	TTGGGATTCT	TTCCATTATG	ATTCTTTGTT	ACAGGCACCG	960
AGATGTTCTA	GA					972

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	885 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single
(D)	TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

ATGCAGCAGC	CCATGAATTA	CCCATGTCCC	CAGATCTTCT	GGGTAGACAG	CAGTGCCACT	60
TCATCTTGGG	CTCCTCCAGG	GTCAGTTTTT	CCCTGTCCAT	CTTGTGGGCC	TAGAGGGCCG	120
GACCAAAGGA	GACCGCCACC	TCCACCACCA	CCTGTGTCAC	CACTACCACC	GCCATCACAA	180
CCACTCCAC	TGCCGCCACT	GACCCCTCTA	AAGAAGAAGG	ACCACAACAC	AAATCTGTGG	240
CTACCGGTGG	TATTTTTTCAT	GGTTCTGGTG	GCTCTGGTTG	GAATGGGATT	AGGAATGTAT	300
CAGCTCTTCC	ACCTGCAGAA	GGAAGTGGCA	GAAGTCCGTG	AGTTCACCAA	CCAAAGCCTT	360
AAAGTATCAT	CTTTTGAAAA	GCAAATAGCC	AACCCAGTA	CACCCTCTGA	AAAAAAGAG	420
CCGAGGAGTG	TGGCCCATTT	AACAGGGAAC	CCCCACTCAA	GGTCCATCCC	TCTGGAATGG	480
GAAGACACAT	ATGGAACCGC	TCTGATCTCT	GGAGTGAAGT	ATAAGAAAGG	TGGCCTTGTG	540
ATCAACGAAG	CTGGGTTGTA	CTTCGTATAT	TCCAAAGTAT	ACTTCCGGGG	TCAGTCTTGC	600
AACAACCAGC	CCCTAAACCA	CAAGGTCTAT	ATGAGGAACT	CTAAGTATCC	TGGGGATCTG	660
GTGCTAATGG	AGGAGAAGAG	GTTGAACTAC	TGCACTACTG	GACAGATATG	GGCCCACAGC	720
AGCTACCTGG	GGGCAGTATT	CAATCTTACC	AGTGCTGACC	ATTTATATGT	CAACATATCT	780
CAACTCTCTC	TGATCAATTT	TGAGGAATCT	AAGACCTTTT	TCGGCTTGTA	TAAGCTTTAA	840
AAGAAAAAGC	ATTTTAAAT	GATCTACTAT	TCTTTATCAT	GGGCA		885

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	29 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single
(D)	TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

CTTAAGCTTC TACAGGACTG AGAAGAAGT

29

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	30 base pairs
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CTTGAAATTCC AACATTCTCG GTGCCTGTAA

27

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	27 base pairs
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

TCAGGATCCA CAAGGCTGTG AGAAGGA

27

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	27 base pairs
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

CTTGTCTAGA CCTGGTGCC CATGATA

27

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 680 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

ATGCCGGAGG	AAGGTCGCCC	TTGCCCCTGG	GTTGCTGGA	GCGGGACCGC	GTTCCAGCGC	60
CAATGGCCAT	GGCTGCTGCT	GGTGGTGT	TTTACTGTGT	TTTGCTGTTG	GTTCATTGT	120
AGCGGACTAC	TCAGTAAGCA	GCAACAGAGG	CTGCTGGAGC	ACCCTGAGCC	GCACACAGCT	180
GAGTTACAGC	TGAATCTCAC	AGTTCCTCGG	AAGGACCCCA	CACTGCGCTG	GGGAGCAGGC	240
CCAGCCTTGG	GAAGGTCCTT	CACACACGGA	CCAGAGCTGG	AGGAGGGCCA	TCTGCGTATC	300
CATCAAGATG	GCCTCTACAG	GCTGCATATC	CAGGTGACAC	TGGCCAACTG	CTCTTCCCCA	360
GGCAGCACCC	TGCAGCACAG	GGCCACCCTG	GCTGTGGGCA	TCTGCTCCCC	CGCTGCGCAC	420
GGCATCAGCT	TGCTGCGTGG	GCGCTTTGGA	CAGGACTGTA	CAGTGGCATT	ACAGCGCCTG	480
ACATACCTGG	TCCACGGAGA	TGTCCTCTGT	ACCAACCTCA	CCCTGCCTCT	GCTGCCGTCC	540
CGCAACGCTG	ATGAGACCTT	CTTTGGAGTT	CAGTGGATAT	GCCCTTGACC	ACAACTCCAG	600
GATGACTTGT	GAATATTTT	TTTCTTTTCA	AGTCTACGT	ATTTATAAAT	GTATATAGTA	660
CACATAAAAA	AAAAAAAAAA					680

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 846 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

ATGCAGCAGC	CCTTCAATTA	CCCATATCCC	CAGATCTACT	GGGTGGACAG	CAGTGCCAGC	60
TCTCCCTGGG	CCCCCTCAGG	CACAGTTCTT	CCCTGTCCAA	CCTCTGTGCC	CAGAAGGCCT	120
GGTCAAAGGA	GGCCACCACC	ACCACCGCCA	CCGCCACCAC	TACCACCTCC	GCCGCCGCCG	180
CCACCACTGC	CTCCACTACC	GCTGCCACCC	CTGAAGAAGA	GAGGGAACCA	CAGCACAGGC	240
CTGTGTCTCC	TTGTGATGTT	TTTCATGGTT	CTGGTTGCCT	TGGTAGGATT	GGGCCTGGGG	300
ATGTTTCAGC	TCTTCCACCT	GCAGAAGGAA	CTGGCAGAAC	TCCGTGAGTT	CACCAACCAA	360
AGCCTTAAAG	TATCATCTTT	TGAAAAGCAA	ATAGGCCACC	CCAGTCCACC	CCCTGAAAAA	420
AAGGAGCTGA	GGAAAGTGGC	CCATTTAACA	GGCAAGTCCA	ACTCAAGGTC	CATGCCTCTG	480
GAATGGGAAG	ACACCTATGG	AATTGTCCTG	CTTTCTGGAG	TGAAGTATAA	GAAGGGTGGC	540
CTTGTGATCA	ATGAAACTGG	GCTGTACTTT	GTATATTCCA	AAGTATACTT	CCGGGGTCAA	600
TCTTGCAACA	ACCTGCCCCCT	GAGCCACAAG	GTCTACATGA	GGAACCTCTAA	GTATCCCCAG	660

GATCTGGTGA	TGATGGAGGG	GAAGATGATG	AGCTACTGCA	CTACTGGGCA	GATGTGGGCC	720
CGCAGCAGCT	ACCTGGGGGC	AGTGTTCAT	CTTACCAGTG	CTGATCATT	ATATGTCAAC	780
GTATCTGAGC	TCTCTCTGGT	CAATTTTGAG	GAATCTCAGA	CGTTTTTCGG	CTTATATAAG	840
CTCTAA						846

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	786 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single
(D)	TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

ATGCAGCAGC	CCTTCAATTA	CCCATATCCC	CAGATCTACT	GGGTGGACAG	CAGTGCCAGC	60
TCTCCCTGGG	CCCCTCCAGG	CACAGTTCTT	CCCTGTCCAA	CCTCTGTGCC	CAGAAGGCCT	120
GGTCAAAGGA	GGCCACCACC	ACCACCGCCA	CCGCCACCAC	TACCACCTCC	GCCGCCGCCG	180
CCACCACTGC	CTCCACTACC	GCTGCCACCC	CTGAAGAAGA	GAGGGAACCA	CAGCACAGGC	240
CTGTGTCTCC	TTGTGATGTT	TTTCATGGTT	CTGGTTGCCT	TGGTAGGATT	GGGCCTGGGG	300
ATGTTTCAGC	TCTTCCGCTT	CGCACAGGCT	ATAGGCCACC	CCAGTCCACC	CCCTGAAAAA	360
AAGGAGCTGA	GGAAAGTGGC	CCATTTAACA	GGCAAGTCCA	ACTCAAGGTC	CATGCCTCTG	420
GAATGGGAAG	ACACCTATGG	AATTGTCTTG	CTTTCTGGAG	TGAAGTATAA	GAAGGGTGGC	480
CTTGTGATCA	ATGAAACTGG	GCTGTACTTT	GTATATTCCA	AAGTATACTT	CCGGGGTCAA	540
TCTTGCAACA	ACCTGCCCCCT	GAGCCACAAG	GTCTACATGA	GGAACCTCTA	GTATCCCCAG	600
GATCTGGTGA	TGATGGAGGG	GAAGATGATG	AGCTACTGCA	CTACTGGGCA	GATGTGGGCC	660
CGCAGCAGCT	ACCTGGGGGC	AGTGTTCAT	CTTACCAGTG	CTGATCATT	ATATGTCAAC	720
GTATCTGAGC	TCTCTCTGGT	CAATTTTGAG	GAATCTCAGA	CGTTTTTCGG	CTTATATAAG	780
CTCTAA						846

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	864 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single
(D)	TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

ATGCAGCAGC	CCTTCAATTA	CCCATATCCC	CAGATCTACT	GGGTGGACAG	CAGTGCCAGC	60
TCTCCCTGGG	CCCCTCCAGG	CACAGTTCTT	CCCTGTCCAA	CCTCTGTGCC	CAGAAGGCCT	120
GGTCAAAGGA	GGCCACCACC	ACCACCGCCA	CCGCCACCAC	TACCACCTCC	GCCGCCGCCG	180
CCACCACTGC	CTCCACTACC	GCTGCCACCC	CTGAAGAAGA	GAGGGAACCA	CAGCACAGGC	240

CTGTGTCTCC	TTGTGATGTT	TTTCATGGTT	CTGGTTGCCT	TGGTAGGATT	GGGCCTGGGG	300
ATGTTTCAGC	TCTTCCAATC	CTCCATCCTC	CCCTATGCCG	GAGGAGGGTT	CGGGCTGCTC	360
GGTGCGGGCG	AGGCCCTATG	GGTGCGTCCT	GCGGCCATCC	TCAATCCTAT	AGGCCACCCC	420
AGTCCACCCC	CTGAAAAAAA	GGAGCTGAGG	AAAGTGGCCC	ATTTAACAGG	CAAGTCCAAC	480
TCAAGGTCCA	TGCCTCTGGA	ATGGGAAGAC	ACCTATGGAA	TTGTCCTGCT	TTCTGGAGTG	540
AAGTATAAGA	AGGGTGGCCT	TGTGATCAAT	GAAACTGGGC	TGTACTTTGT	ATATTCCAAA	600
GTATACTTCC	GGGGTCAATC	TTGCAACAAC	CTGCCCCTGA	GCCACAAGGT	CTACATGAGG	660
AACTCTAAGT	ATCCCCAGGA	TCTGGTGATG	ATGGAGGGGA	AGATGATGAG	CTACTGCACT	720
ACTGGGCAGA	TGTGGGCCCC	CAGCAGCTAC	CTGGGGGCAG	TGTTCAATCT	TACCAGTGCT	780
GATCATTTAT	ATGTCAACGT	ATCTGAGCTC	TCTCTGGTCA	ATTTTGAGGA	ATCTCAGACG	840
TTTTTCGGCT	TATATAAGCT	CTAA				864

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	828 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single
(D)	TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

ATGCAGCAGC	CCTTCAATTA	CCCATATCCC	CAGATCTACT	GGGTGGACAG	CAGTGCCAGC	60
TCTCCCTGGG	CCCCTCCAGG	CACAGTTCTT	CCCTGTCCAA	CCTCTGTGCC	CAGAAGGCCT	120
GGTCAAAGGA	GGCCACCACC	ACCACCGCCA	CCGCCACCAC	TACCACCTCC	GCCGCCGCCG	180
CCACCACTGC	CTCCACTACC	GCTGCCACCC	CTGAAGAAGA	GAGGGAACCA	CAGCACAGGC	240
CTGTGTCTCC	TTGTGATGTT	TTTCATGGTT	CTGGTTGCCT	TGGTAGGATT	GGGCCTGGGG	300
ATGTTTCAGC	TCTTCCACCT	ACAGCGAGAG	TCTACCAGCC	AGATGCACAC	AGCATCATCT	360
TTGGAGAAGC	AAATAGGCCA	CCCCAGTCCA	CCCCCTGAAA	AAAAGGAGCT	GAGGAAAGTG	420
GCCCATTATA	CAGGCAAGTC	CAACTCAAGG	TCCATGCCTC	TGGAATGGGA	AGACACCTAT	480
GGAATTGTCC	TGCTTTCTGG	AGTGAAGTAT	AAGAAGGGTG	GCCTTGTGAT	CAATGAAACT	540
GGGCTGTACT	TTGTATATTC	CAAAGTATAC	TTCCGGGGTC	AATCTTGCAA	CAACCTGCCC	600
CTGAGCCACA	AGGTCTACAT	GAGGAACTCT	AAGTATCCCC	AGGATCTGGT	GATGATGGAG	660
GGGAAGATGA	TGAGCTACTG	CACTACTGGG	CAGATGTGGG	CCCGCAGCAG	CTACCTGGGG	720
GCAGTGTTC	ATCTTACCAG	TGCTGATCAT	TTATATGTCA	ACGTATCTGA	GCTCTCTCTG	780
GTCAATTTTG	AGGAATCTCA	GACGTTTTTC	GGCTTATATA	AGCTCTAA		828

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	846 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single
(D)	TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

ATGGCTATGA	TGGAGGTCCA	GGGGGGACCC	AGCCTGGGAC	AGACCTGCGT	GCTGATCGTG	60
ATCTTCACAG	TGCTCCTGCA	GTCTCTCTGT	GTGGCTGTAA	CTTACGTGTA	CTTTACCAAC	120
GAGCTGAAGC	AGATGCAGGA	CAAGTACTCC	AAAAGTGGCA	TTGCTTGTTT	CTTAAAAGAA	180
GATGACAGTT	ATTGGGACCC	CAATGACGAA	GAGAGTATGA	ACAGCCCCTG	CTGGCAAGTC	240
AAGTGGCAAC	TCCGTCAGCT	CGTTAGAAAG	ATGATTTTGA	GAACCTCTGA	GGAAACCATT	300
TCTACAGTTC	AAGAAAAGCA	ACAAAATATT	TCTCCCCTAG	TGAGAGAAAG	AGGTCCCTCAG	360
AGAGTAGCAG	CTCACATAAC	TGGGACCAGA	GGAAGAAGCA	ACACATTGTC	TTCTCCAAAC	420
TCCAAGAATG	AAAAGGCTCT	GGGCCGCAAA	ATAAACTCCT	GGGAATCATC	AAGGAGTGGG	480
CATTCAATTCC	TGAGCAACTT	GCACTTGAGG	AATGGTGAAC	TGGTCATCCA	TGAAAAAGGG	540
TTTTACTACA	TCTATTCCCA	AACATACTTT	CGATTTTCAGG	AGGAAATAAA	AGAAAACACA	600
AAGAACGACA	AACAAATGGT	CCAATATATT	TACAAATACA	CAAGTTATCC	TGACCCTATA	660
TTGTTGATGA	AAAGTGCTAG	AAATAGTTGT	TGGTCTAAAG	ATGCAGAATA	TGGACTCTAT	720
TCCATCTATC	AAGGGGGAAT	ATTTGAGCTT	AAGGAAAATG	ACAGAATTTT	TGTTTCTGTA	780
ACAAATGAGC	ACTTGATAGA	CATGGACCAT	GAAGCCAGTT	TTTTCGGGGC	CTTTTTAGTT	840
GGCTAA						846

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	876 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single
(D)	TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

ATGCCTTCCT	CAGGGGCCCT	GAAGGACCTC	AGCTTCAGTC	AGCACTTCAG	GATGATGGTG	60
ATTTGCATAG	TGCTCCTGCA	GGTGCTCCTG	CAGGCTGTGT	CTGTGGCTGT	GACTTACATG	120
TACTTCACCA	ACGAGATGAA	GCAGCTGCAG	GACAATTACT	CCAAAATTGG	ACTAGCTTGC	180
TTCTCAAAGA	CGGATGAGGA	TTTCTGGGAC	TCCACTGATG	GAGAGATCTT	GAACAGACCC	240
TGCTTGACAG	TTAAGAGGCA	ACTGTATCAG	CTCATTGAAG	AGGTGACTTT	GAGAACCCTTT	300
CAGGACACCA	TTTCTACAGT	TCCAGAAAAG	CAGCTAAGTA	CTCCTCCCTT	GCCCAGAGGT	360
GGAAGACCTC	AGAAAGTGGC	AGCTCACATT	ACTGGGATCA	CTCGGAGAAG	CAACTCAGCT	420
TTAATTCCAA	TCTCCAAGGA	TGGAAAGACC	TTAGGCCAGA	AGATTGAATC	CTGGGAGTCC	480
TCTCGGAAAG	GGCATTTCATT	TCTCAACCAC	GTGCTCTTTA	GGAATGGAGA	GCTGGTCATC	540
GAGCAGGAGG	GCCTGTATTA	CATCTATTCC	CAAACATACT	TCCGATTTCA	GGAAGCTGAA	600
GACGCTTCCA	AGATGGTCTC	AAAGGACAAG	GTGAGAACCA	AACAGCTGGT	GCAGTACATC	660
TACAAGTACA	CCAGCTATCC	GGATCCCAT	GTGCTCATGA	AGAGCGCCAG	AAACAGCTGT	720
TGGTCCAGAG	ATGCCGAGTA	CGGACTGTAC	TCCATCTATC	AGGGAGGATT	GTTCGAGCTA	780
AAAAAAAATG	ACAGGATTTT	TGTTTCTGTG	ACAAATGAAC	ATTTGATGGA	CCTGGATCAA	840
GAAGCCAGCT	TCTTTGGAGC	CTTTTAAATT	AACTAA			876

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 720 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

ATGGAGCCAG	GGCTGCAACA	AGCAGGCAGC	TGTGGGGGCTC	CTTCCCCCTGA	CCCAGCCATG	60
CAGGTGCAGC	CCGGCTCGGT	AGCCAGCCCC	TGGAGAAGCA	CGAGGCCCTG	GAGAAGCACA	120
AGTCGCAGCT	ACTTCTACCT	CAGCACCACC	GCACTGGTGT	GCCTTGTTGT	GGCAGTGGCG	180
ATCATTCTGG	TACTGGTAGT	CCAGAAAAAG	GACTCCACTC	CAAATACAAC	TGAGAAGGCC	240
CCCCTTAAAG	GAGGAAATTG	CTCAGAGGAT	CTCTTCTGTA	CCCTGAAAAAG	TACTCCATCC	300
AAGAAGTCAT	GGGCTTACCT	CCAAGTGTC	AAGCATCTCA	ACAATACCAA	ACTGTCATGG	360
AACGAAGATG	GCACCATCCA	CGGACTCATA	TACCAGGACG	GGAACCTGAT	AGTCCAATTC	420
CCTGGCTTGT	ACTTCATCGT	TTGCCAACTG	CAGTTCCTCG	TGCAGTGCTC	AAATCATTCT	480
GTGGACCTGA	CATTGCAGCT	CCTCATCAAT	TCCAAGATCA	AAAAGCAGAC	GTTGGTAACA	540
GTGTGTGAGT	CTGGAGTTCA	GAGTAAGAAC	ATCTACCAGA	ATCTCTCTCA	GTTTTTGCTG	600
CATTACTTAC	AGGTCAATC	TACCATATCA	GTCAGGGTGG	ATAATTTCCA	GTATGTGGAT	660
ACAAACACTT	TCCCTCTTGA	TAATGTGCTA	TCCGTCTTCT	TATATAGTAG	CTCAGACTGA	720

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 930 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

ATGGACCAGC	ACACACTTGA	TGTGGAGGAT	ACCGCGGATG	CCAGACATCC	AGCAGGTACT	60
TCGTGCCCCCT	CGGATGCGGC	GCTCCTCAGA	GATACCGGGC	TCCTCGCGGA	CGCTGCGCTC	120
CTCTCAGATA	CTGTGCGCCC	CACAAATGCC	GCGCTCCCCA	CGGATGCTGC	CTACCCTGCG	180
GTTAATGTTT	GGGATCGCGA	GGCCGCGTGG	CCGCTGCAC	TGAACTTCTG	TTCCCGCCAC	240
CCAAAGCTCT	ATGGCCTAGT	CGCTTTGGTT	TTGCTGCTTC	TGATCGCCGC	CTGTGTTCCCT	300
ATCTTCACCC	GCACCGAGCC	TCGGCCAGCG	CTCACAATCA	CCACCTCGCC	CAACCTGGGT	360
ACCCGAGAGA	ATAATGCAGA	CCAGGTCACC	CCTGTTTCCC	ACATTGGCTG	CCCCAACACT	420
ACACAACAGG	GCTCTCCTGT	GTTCCGCAAG	CTACTGGCTA	AAAACCAAGC	ATCGTTGTGC	480
AATACAATC	TGAAGTGGCA	CAGCCAAGAT	GGAGCTGGGA	GCTCATACCT	ATCTCAAGGT	540
CTGAGGTACG	AAGAAGACAA	AAAGGAGTTG	GTGGTAGACA	GTCCCGGGCT	CTACTACGTA	600
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GTGGAACTGT	TCCCTTGCTC	CATGGAGAAC	AAGTTAGTGG	ACCGTTCCTG	GAGTCAACTG	780
TTGCTCCTGA	AGGCTGGCCA	CCGCCTCAGT	GTGGGTCTGA	GGGCTTATCT	GCATGGAGCC	840
CAGGATGCAT	ACAGAGACTG	GGAGCTGTCT	TATCCCAACA	CCACCAGCTT	TGGACTCTTT	900
CTTGTGAAAC	CCGACAACCC	ATGGGAATGA				930

SSSD/66239. v01

CLAIMS

1. A method of altering the immunoreactivity of human cells, which method comprising introducing a gene
5 encoding an accessory molecule ligand into said cells so that said accessory molecule ligand is expressed on the surface of said cells.
2. The method of claim 1 wherein the accessory molecule to which the accessory molecule ligand
10 specifically binds is also present on the surface of said human cells.
3. The method of claim 1 wherein said human cells are neoplastic human cells.
4. The method of claim 1 wherein said accessory
15 molecule ligand gene is a chimeric gene.
5. The method in claim 1 wherein said accessory molecule ligand gene is present in a vector capable of transducing human cells.
6. The method of claim 1 wherein said accessory
20 molecule ligand gene is present as part of a genetic vector.
7. The method of claim 1 wherein said accessory molecule ligand gene is operatively linked to a promoter region and a polyadenylation signal.
- 25 8. The method of claim 1 wherein said gene is a CD40 ligand gene.
9. The method of claim 7 wherein said CD40 ligand gene is a murine CD40 ligand gene.
10. The method of claim 4 wherein said gene is a
30 chimeric gene which comprises at least a portion of a murine CD40 ligand gene.
11. A method of treating a human neoplasia comprising inserting into said human neoplastic cells a gene which

encodes an accessory molecule ligand into said human neoplastic cells so that said accessory molecule ligand is expressed on the surface of said neoplastic cells.

12. The method of claim 11 further comprising:

5 a) obtaining said human neoplastic cells from a human patient;

 b) infusing said human neoplastic cells after having inserted said accessory molecule ligand on the surface of said cells back into said patient.

10 13. The method of claim 11 wherein the accessory molecule to which the said accessory molecule ligand specifically binds is present on the surface of said human neoplastic cells.

 14. The method of claim 11 wherein said accessory molecule ligand gene is a chimeric gene.

 15. The method of claim 11 wherein said accessory molecule ligand gene is a chimeric gene which contains at least a portion of the murine CD40 ligand gene.

20 16. The method of claim 11 wherein said accessory molecule ligand gene is present as part of a genetic vector.

 17. The method of claim 11 wherein said accessory molecule ligand gene is operatively linked to a promoter region and a 3' end region.

25 18. The method of claim 11 wherein said accessory molecule ligand gene is a CD40 ligand gene.

 19. The method of claim 11 wherein the said CD40 ligand gene is a murine CD40 ligand gene.

30 20. The method of claim 11 wherein said accessory molecule ligand gene is a Fas-ligand gene or a CD27 ligand gene.

 21. The method of claim 11 wherein said accessory molecule ligand gene is present in a gene therapy vector.

22. A method of treating a neoplasia in a patient comprising injecting into the tumor bed of said patient a gene which encodes an accessory molecule ligand so that said accessory molecule ligand is expressed on the surface
5 of said tumor cells thereby causing said cells to participate in an immune reaction.

23. A gene therapy vector containing an accessory molecule ligand gene.

24. The gene therapy vector of claim 23 wherein said
10 accessory molecule gene is a CD40 ligand gene.

25. The gene therapy vector of claim 23 wherein said CD40 ligand gene is a murine CD40 ligand gene.

26. The gene therapy vector of claim 23 wherein said CD40 ligand gene is a chimeric gene.

15 27. The gene therapy vector of claim 23 wherein said chimeric gene contains at least a portion of the murine CD40 ligand gene.

28. The gene therapy vector of claim 23 wherein at least a portion of said vector is derived from adenovirus
20 DNA.

29. The gene therapy vector of claim 23 wherein said vector contains at least a promoter region and a 3' end region.

30. The gene therapy vector of claim 23 wherein said
25 promoter region and said 3' end region are not derived from the same species from which the CD40 ligand gene is derived.

31. The gene therapy vector of claim 23 wherein said portion of said vector is derived from viral DNA.

30 32. The gene therapy vector of claim 23 wherein at least a portion of said vector is derived from a retrovirus.

33. The gene therapy vector of claim 23 wherein said vector is capable of transducing human cells.

34. The gene therapy vector of claim 23 wherein said vector is capable of transducing animal cells.

5 35. The gene therapy vector of claim 23 wherein said human cells are human neoplastic cells.

36. The gene therapy vector of claim 23 wherein said human cells are human antigen presenting cells.

37. A genetic construct containing a promoter
10 operatively linked to an accessory molecule ligand gene which is also operatively linked to a polyadenylation signal.

38. A genetic construct in which a promoter is
15 operatively linked to a chimeric accessory molecule ligand gene and a polyadenylation signal.

39. A gene therapy vector containing a chimeric accessory molecule ligand gene.

40. The gene therapy vector of claim 39 wherein said
20 chimeric accessory molecule ligand gene contains at least one gene segment derived from a murine CD40 ligand gene and other gene segments derived from other accessory molecule genes.

41. The gene therapy vector of claim 39 wherein said
25 other accessory molecule ligand genes are human accessory molecule ligand genes.

42. The gene therapy vector of claim 39 wherein said human accessory molecule ligand genes are human CD40 ligand genes

43. A human cell containing the gene therapy vector
30 of claims 23-36 or 39-42 or the genetic construct of claims 37-38.

44. The human cell of claim 43 wherein said cell is an antigen presenting cell.

45. The human cell of claim 43 wherein said human cell is a neoplastic cell.

46. The human cell of claim 43 wherein said cell is an accessory cell.

5 47. An animal cell containing the gene therapy vector or genetic construct of claims 23-43.

48. An insect cell containing the gene therapy vector or genetic construct of claims 23-43.

10 49. A bacterial cell containing the gene therapy vector or genetic construct of claims 23-43.

50. A method of vaccinating an animal against a predetermined organism comprising: administering into an animal to be immunized against a predetermined organism, a vaccine comprising immunogenic antigens capable of causing
15 an immune response to said predetermined organism together with a vector containing a gene including an accessory molecule ligand.

51. The method of claim 50 wherein said immunogenic antigens are encoded by genes present on a genetic vector.

20 52. The method of claim 50 wherein said gene is a chimeric gene.

53. The method of claim 50 wherein said chimeric gene contains at least a portion of a murine CD40 ligand gene.

25 54. The method of claim 50 wherein said chimeric gene contains at least a segment of a murine CD40 ligand gene and at least a segment of a different accessory molecule gene.

30 55. The method of claim 50 wherein said predetermined organism is a virus, a bacteria, a fungus or a neoplastic cell.

56. A method of producing an immune response directed to a predetermined antigen comprising: administering to said animal a genetic vector containing a gene encoding the

antigen to which said immune response is desired together with a genetic vector containing a gene encoding an accessory molecule ligand gene.

57. A chimeric accessory molecule ligand gene
5 comprising at least one domain or sub-domain gene segment derived from a first accessory molecule ligand gene operatively linked to the domain or sub-domain gene segment of a second accessory molecule ligand gene.

58. The chimeric accessory molecule ligand gene of
10 claim 57 in which said first and second accessory molecule ligand genes are selected from the group consisting of the genes from any species encoding a member of the tumor necrosis family, CD40-ligand, Fas-ligand, CD70, TNF α , TNF β , CD30 ligand, 4-1BB ligand (4-1BBL), TNF-related apoptosis
15 inducing ligand (TRAIL) and nerve growth factor.

59. The chimeric accessory molecule ligand gene of claim 57 in which at least one of said domain or sub-domain gene segments is an artificial gene segment.

60. The chimeric accessory molecule encoded by the
20 genes of claims 57-59.

61. A chimeric accessory molecule ligand gene comprising at least a portion of the gene encoding Domains I and II derived from an accessory molecule ligand operatively linked to at least a portion of the gene
25 encoding a Domain of an accessory molecule ligand which in turn is operatively linked to at least a portion of the gene encoding Domain IV of an accessory molecule ligand.

62. The chimeric accessory molecule ligand gene of claim 61 wherein said Domains I and II are derived from the
30 human CD40 ligand gene.

63. The chimeric accessory molecule ligand gene of claim 61 wherein said Domain IV is the human Fas-ligand Domain IV.

64. The chimeric accessory molecule ligand gene of claim 61 wherein said Domain is Domain III of another accessory molecule ligand.

65. The chimeric accessory molecule ligand gene of claim 61 wherein said Domain is a domain from the same accessory molecule ligand.

66. The chimeric accessory molecule ligand gene of claim 61 wherein said Domain is an artificial domain.

67. The method of claim 4 wherein said chimeric gene is a gene of claims 57-60.

68. The method of claim 11 wherein said accessory molecule ligand gene is a chimeric accessory molecule ligand gene of claims 57-60.

69. The gene therapy vector of claim 23 wherein said chimeric gene is a chimeric accessory molecule ligand gene of claims 57-60.

70. A method of treating rheumatoid arthritis in a joint comprising inserting into the joint a vector containing a gene which encodes an accessory molecule ligand so that said accessory molecule ligand is expressed on the surface of cells within the joint.

71. The method of claim 70 wherein said accessory molecule ligand gene is a chimeric accessory molecule ligand gene which is comprised of at least a portion of a human Fas-ligand gene.

72. The method of claim 70 wherein said accessory molecule ligand gene is a chimeric accessory molecule ligand gene which contains at least a portion of the murine Fas-ligand gene.

73. The method of claim 70 wherein said accessory molecule ligand gene is a murine Fas-ligand gene.

74. The method of claim 70 wherein said accessory molecule ligand gene is the murine Fas-ligand gene.

75. The method of claim 70 wherein said accessory molecule ligand gene is a chimeric accessory molecule gene comprised of at least a portion of domain III from the murine Fas-ligand gene and a portion of domain IV from the human Fas-ligand gene.

76. The method of claim 70 wherein said accessory molecule ligand gene is a chimeric accessory molecule ligand gene comprised of a portion of domain III of the human CD70 gene and at least a portion of domain IV of the human Fas-ligand gene.

77. A method of treating rheumatoid arthritis in a joint comprising inserting into the joint cells which have been transformed with a gene which encodes on accessory molecule ligand which is expressed on the surface of said cells.

78. A chimeric accessory molecule ligand comprised of at least a portion of the fourth domain of human Fas-ligand.

79. A chimeric accessory molecule ligand derived from a Fas-ligand in which at least one matrix metalloproteinase cleavage site has been removed.

80. A chimeric accessory molecule ligand comprised of domain III of the Murine Fas-ligand or the human CD70 gene, and domain IV of the human Fas-ligand.

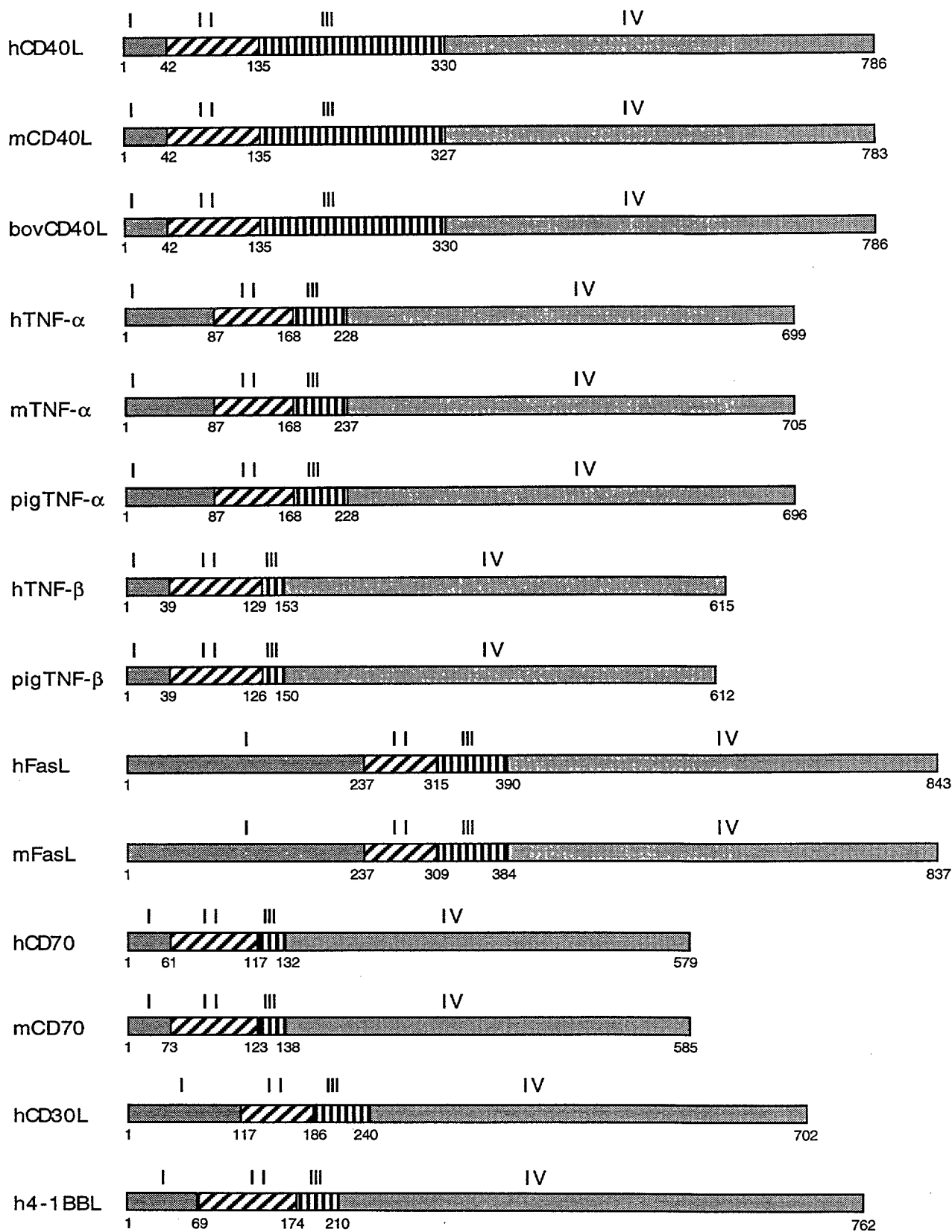
81. A gene therapy vector containing a gene encoding chimeric accessory molecule of claims 78-80.

82. A cell containing a gene therapy vector of claim 81.

83. A method of altering the immunoreactivity of human cells, which method comprising introducing a gene encoding an accessory molecule ligand which has a stabilized activity into said cells so that said accessory molecule ligand is expressed on the surface of said cells.

ABSTRACT

This invention relates to genes which encode accessory molecule ligands and their use for immunomodulation, vaccination and treatments of various human diseases, including malignancies and autoimmune diseases. This invention also describes the use of accessory molecule ligands which are made up of various domains and subdomain portions of molecules derived from the tumor necrosis factor family. The chimeric molecules of this invention contain unique properties which lead to the stabilization of their activities and thus greater usefulness in the treatment of diseases. Vectors for expressing genes which encode the accessory molecule ligands of this invention are also disclosed.



DOMAINS: I - Cytoplasmic Domain; II - Transmembrane Domain; III - Proximal Extracellular Domain; IV - Distal Extracellular Domain (putative soluble form)

Figure 1

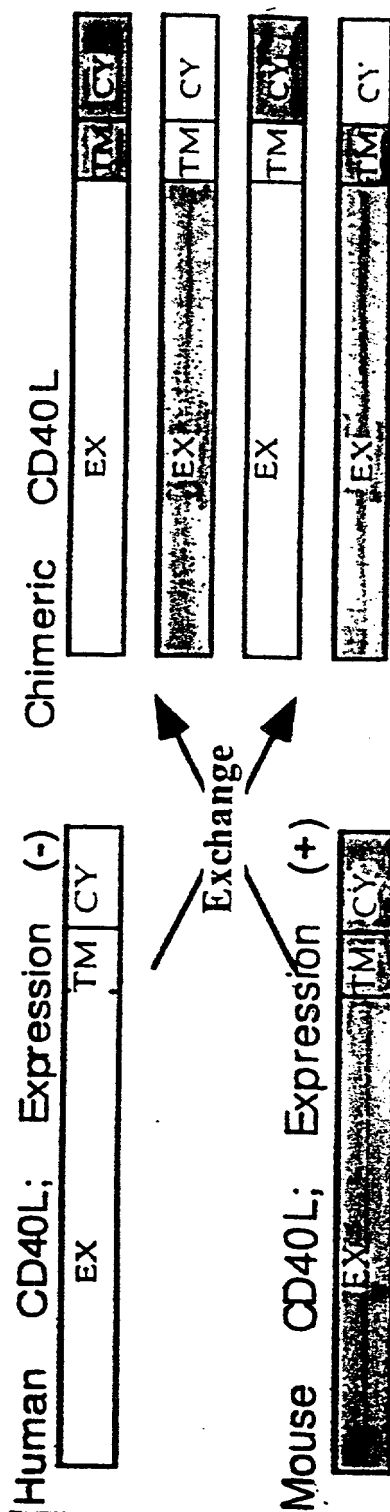


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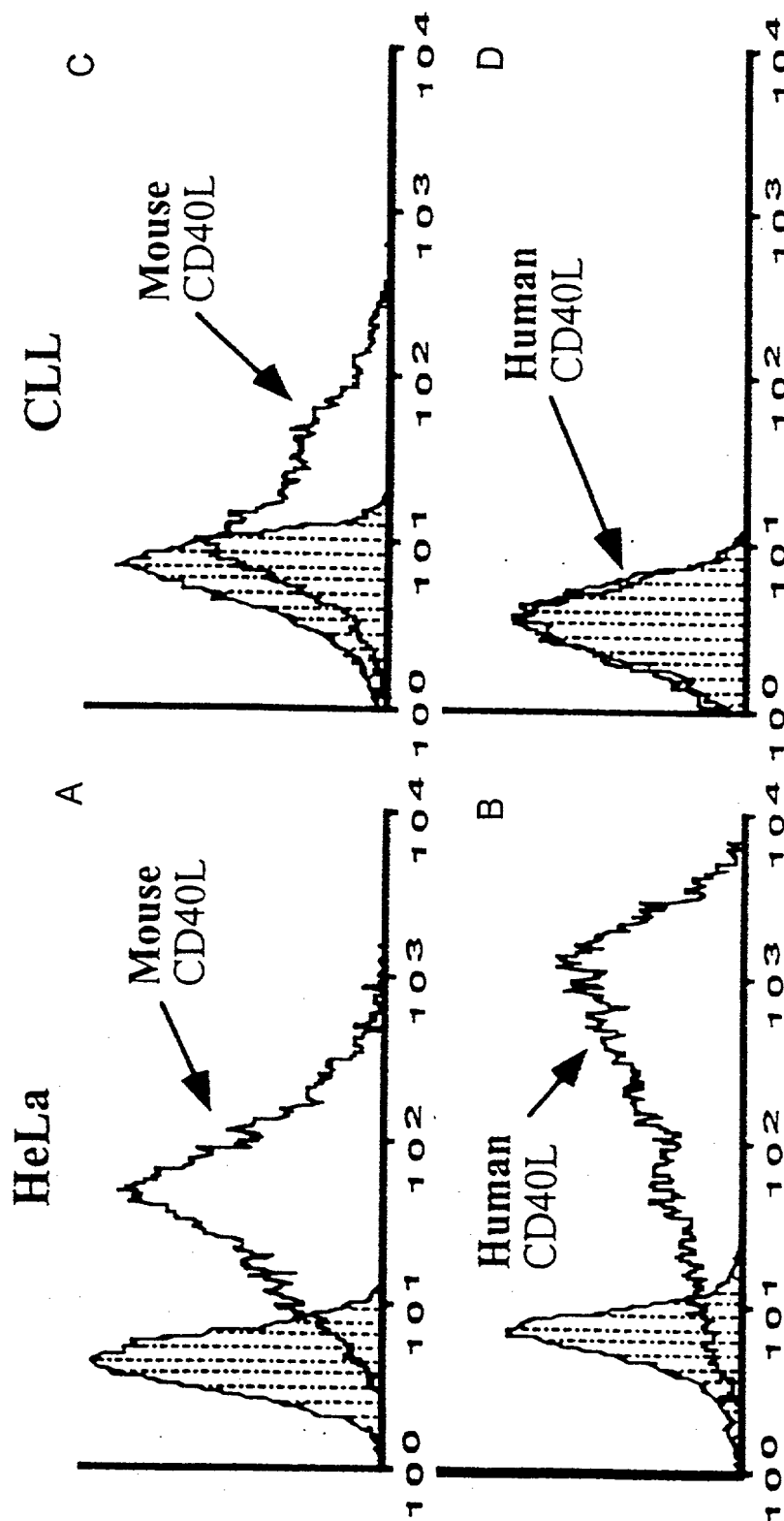
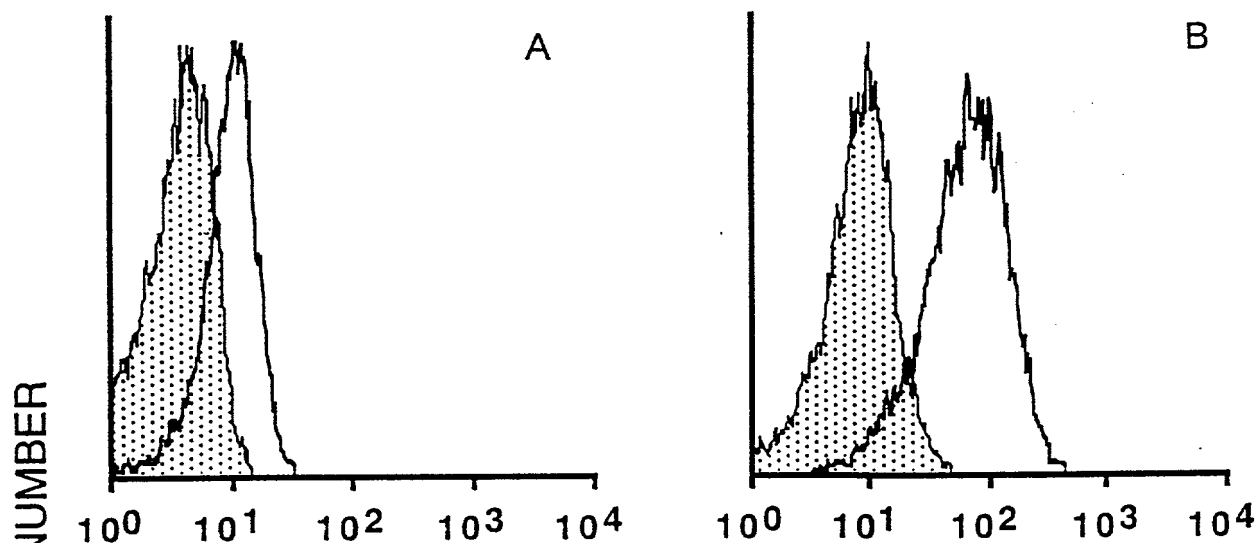


Figure 3

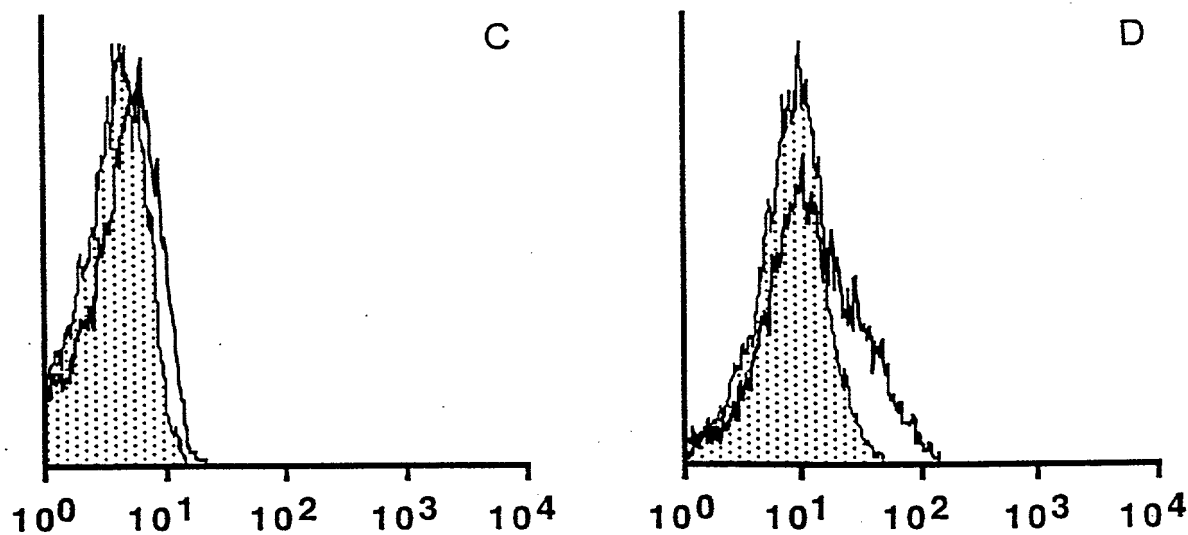
NONINFECTED

+mCD40-L ADENOVIRUS

CD54 EXPRESSION



CD80 EXPRESSION



RELATIVE FLUORESCENCE INTENSITY

Figure 4

Allogenic T cell response to CLL cells transfected with adeno-mCD40L

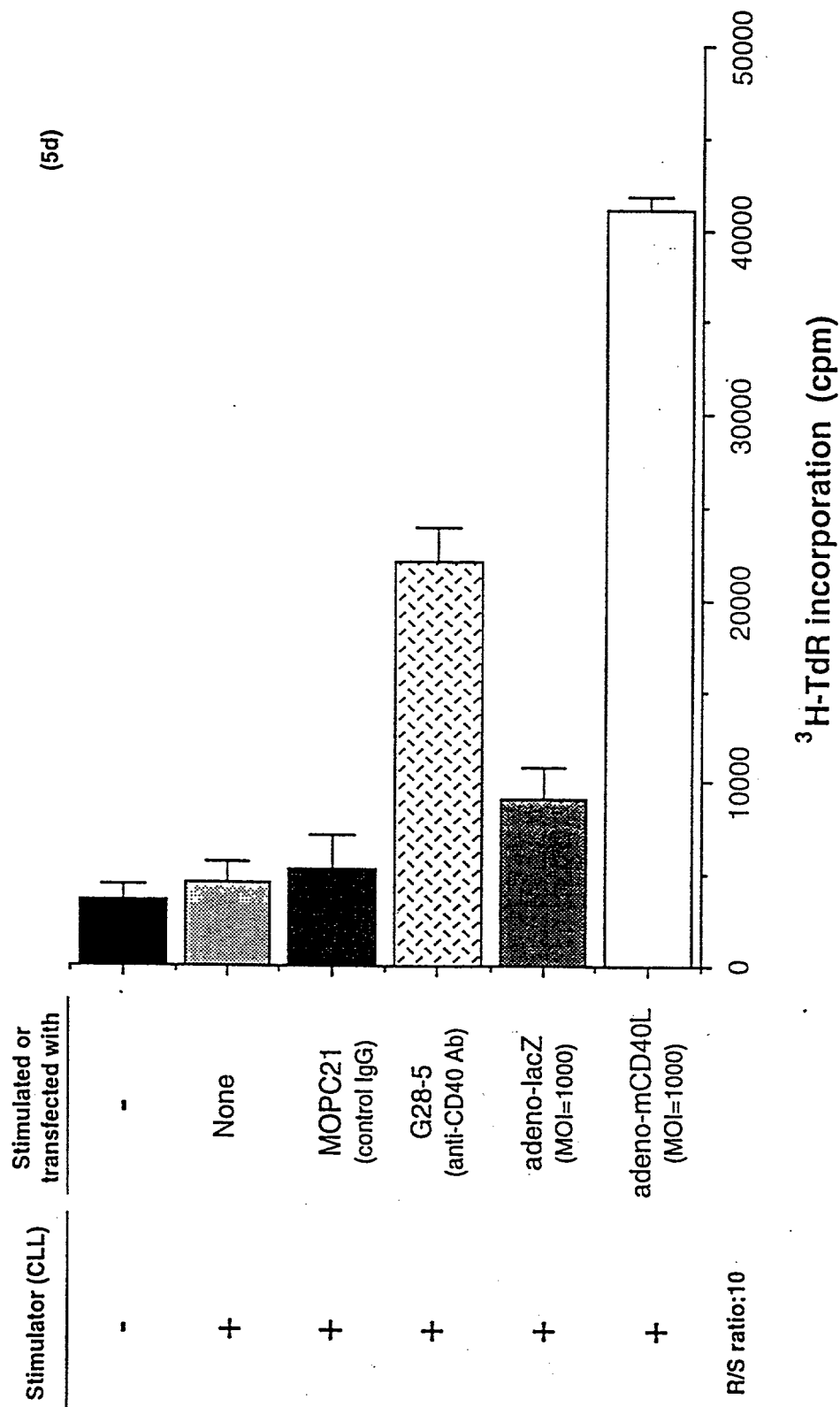


Figure 5

Production of IFN γ by allogenic T lymphocytes stimulated with CLL B cells

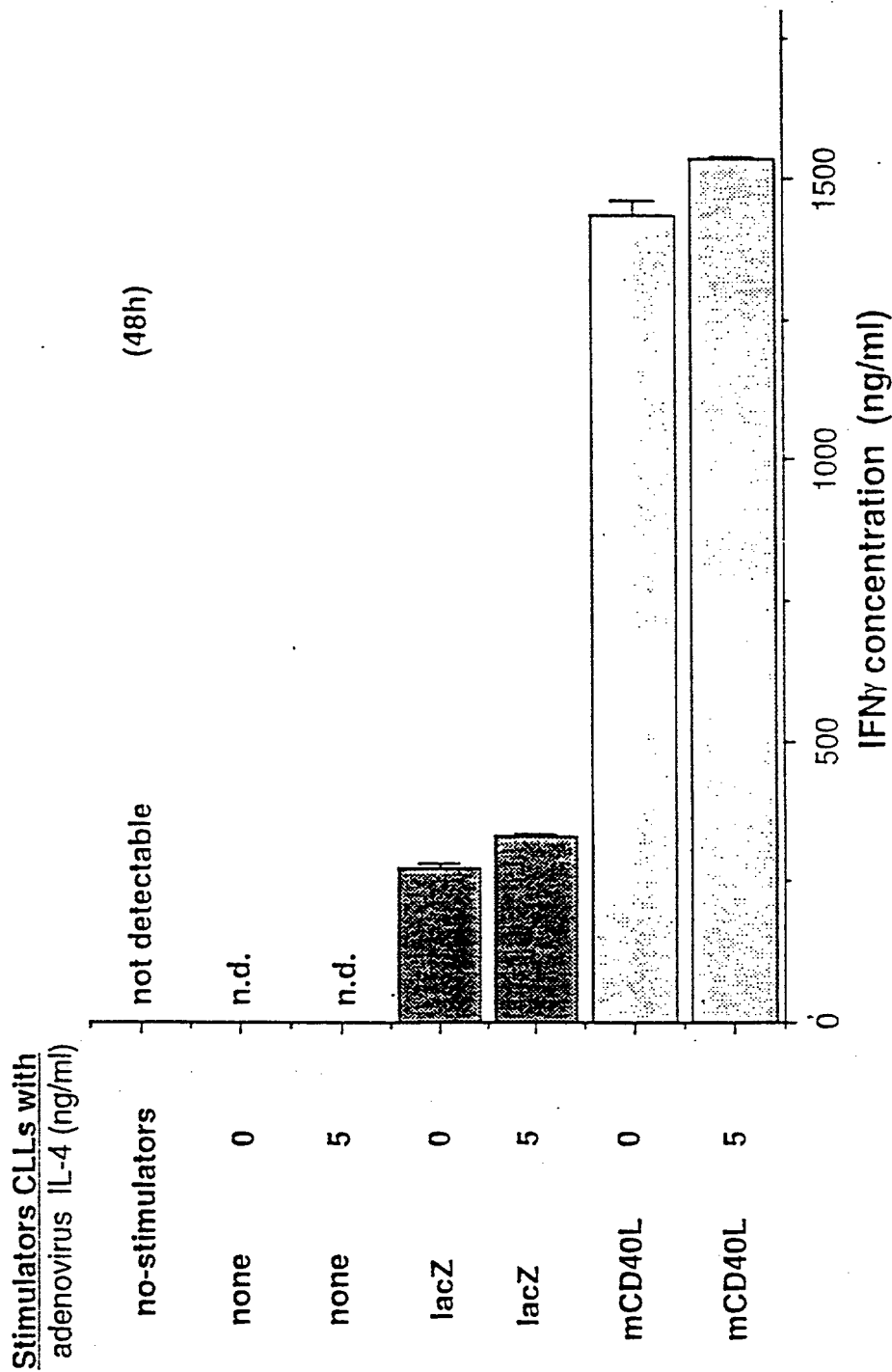


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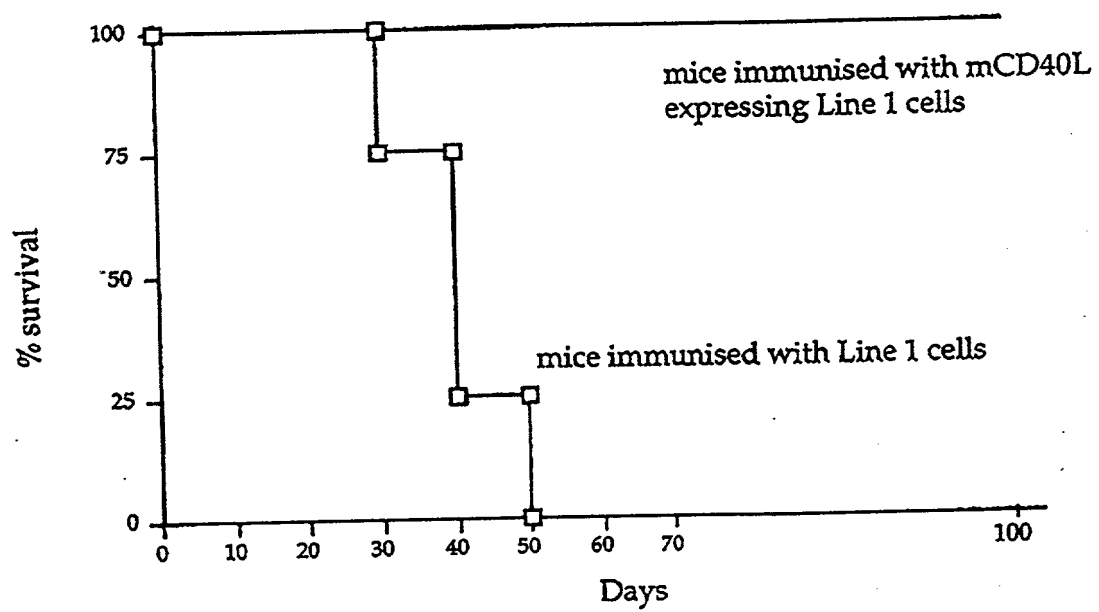


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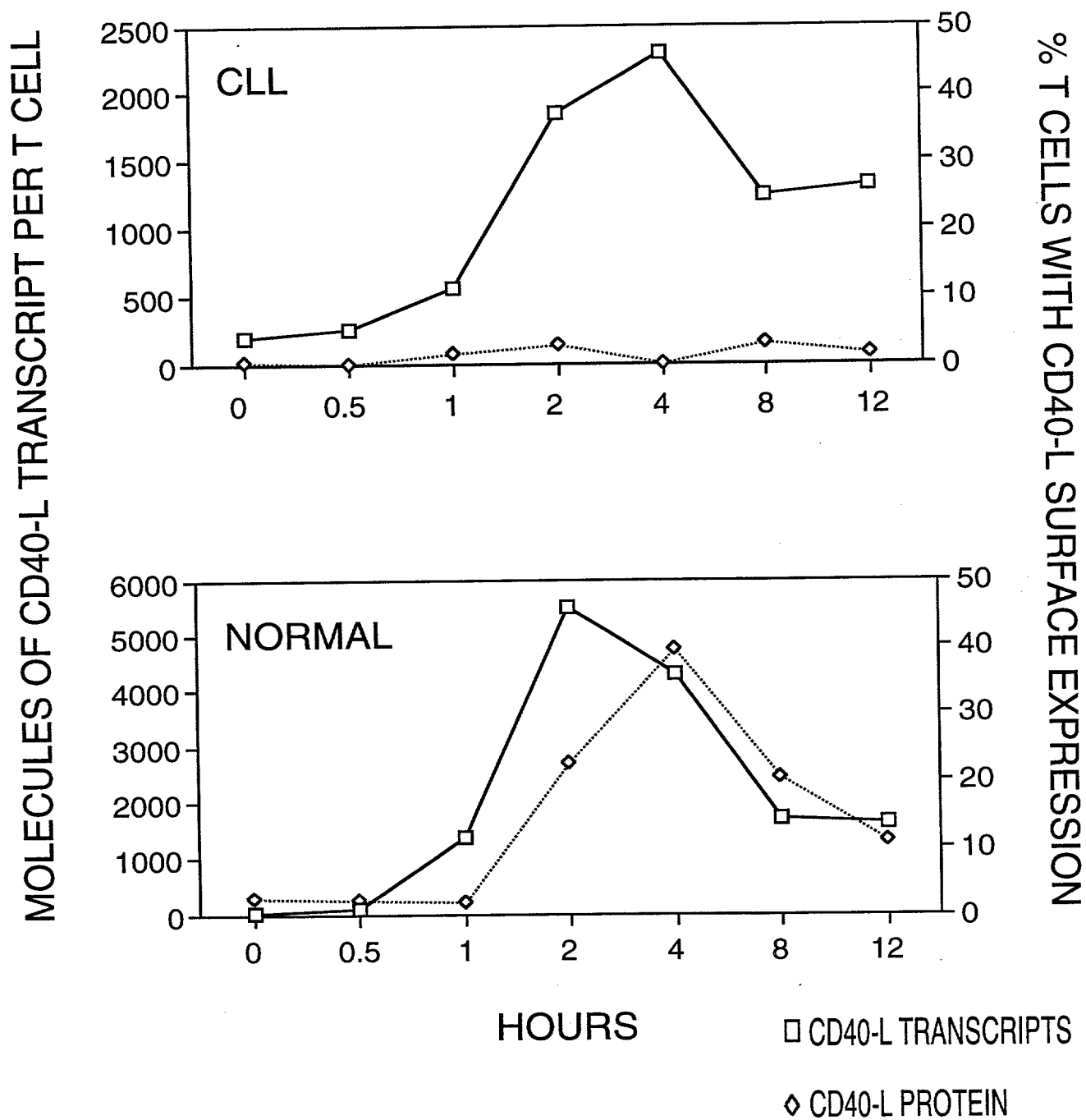


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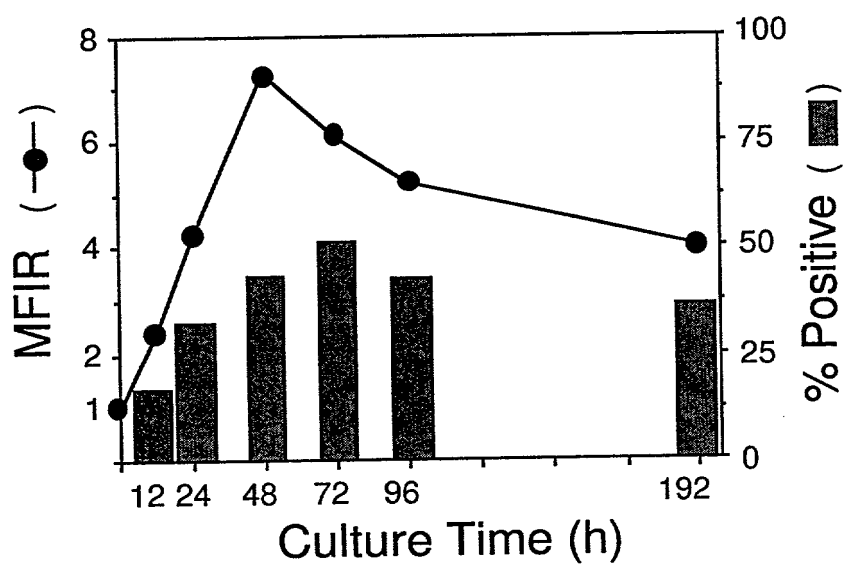


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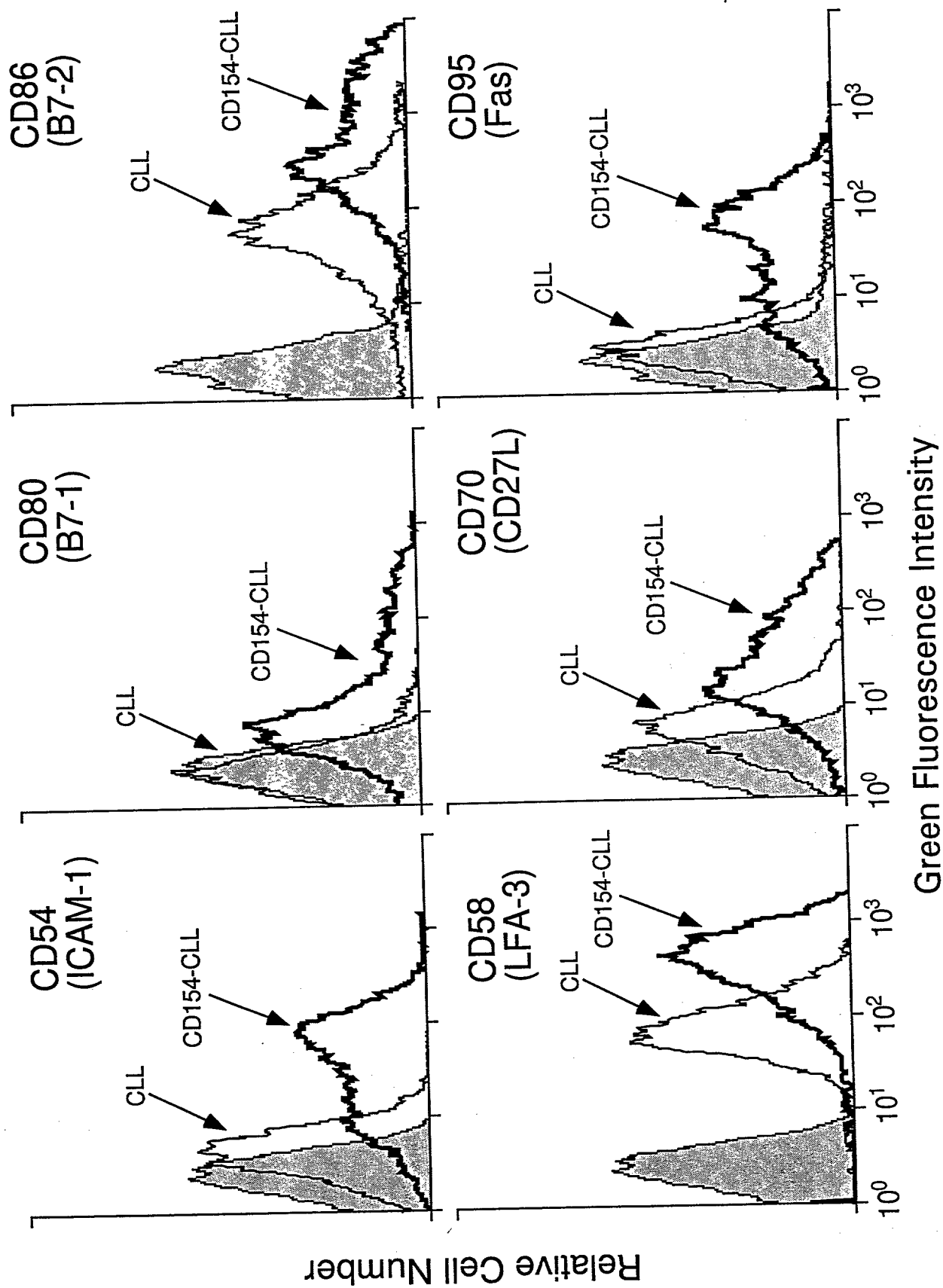


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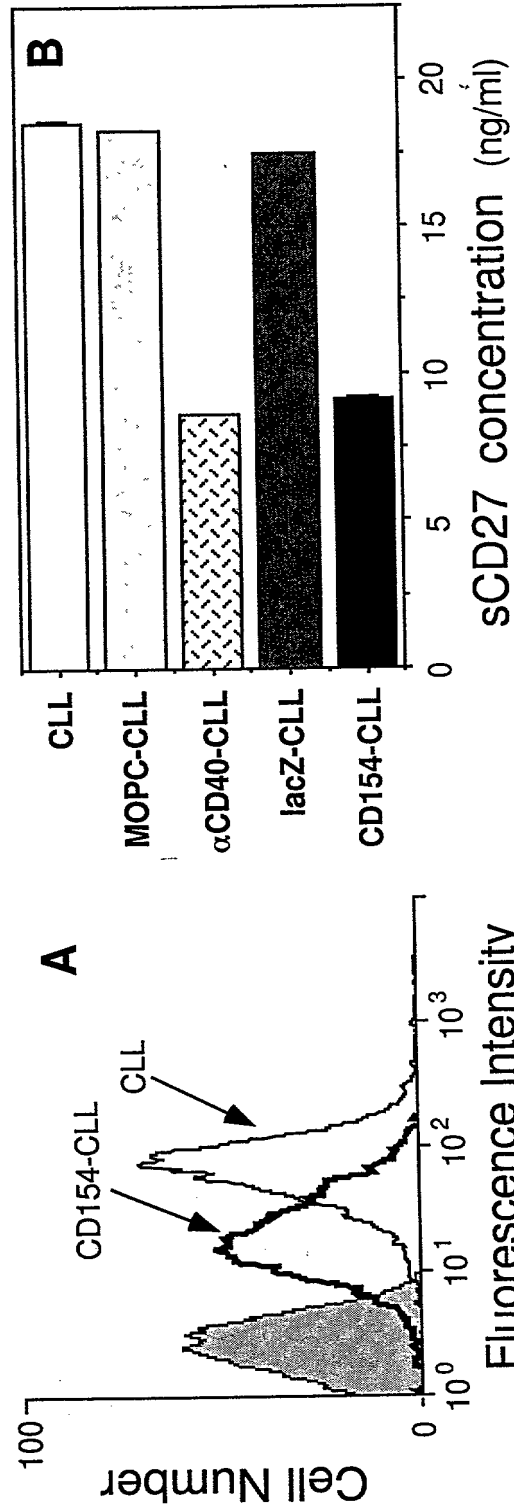


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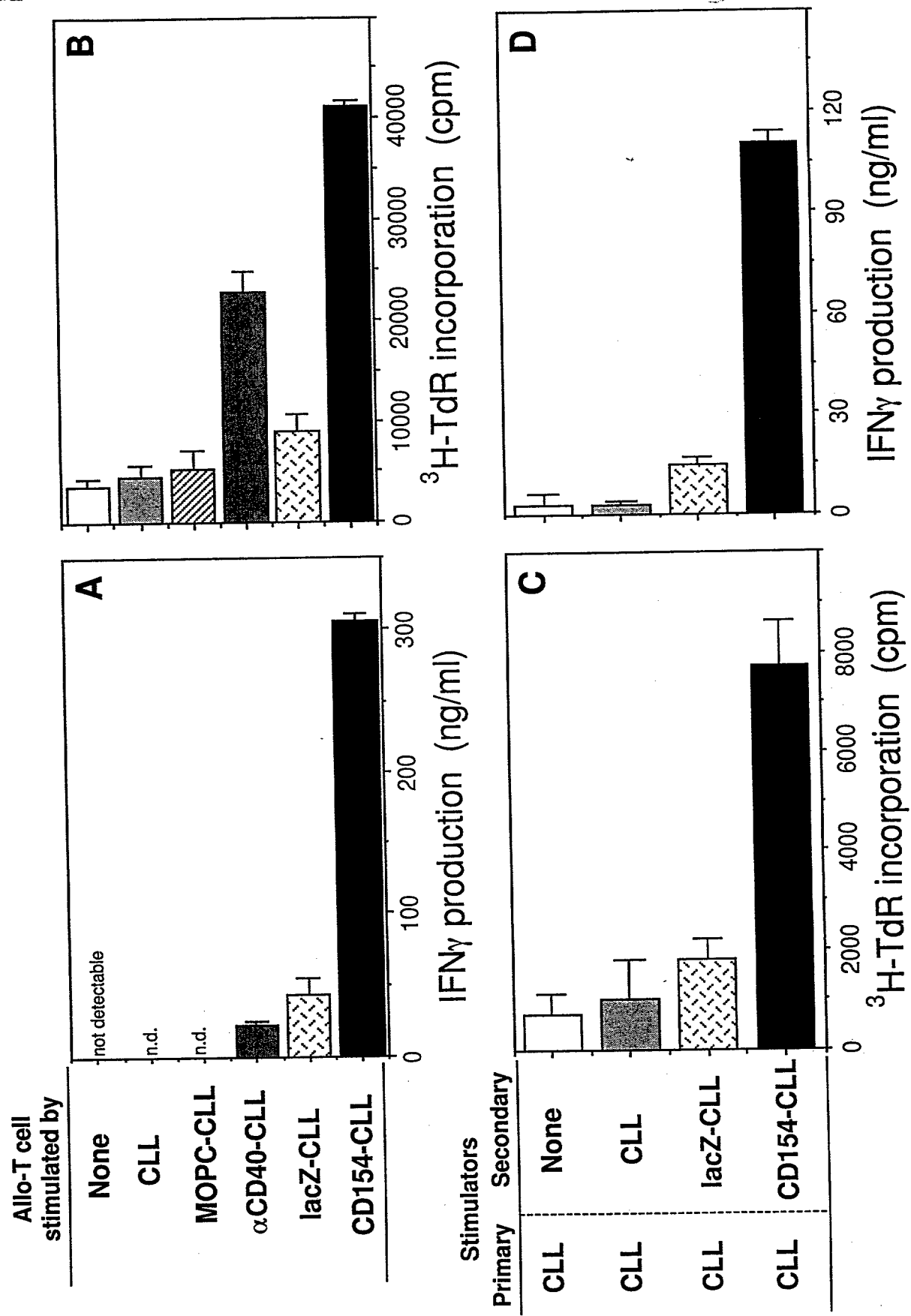


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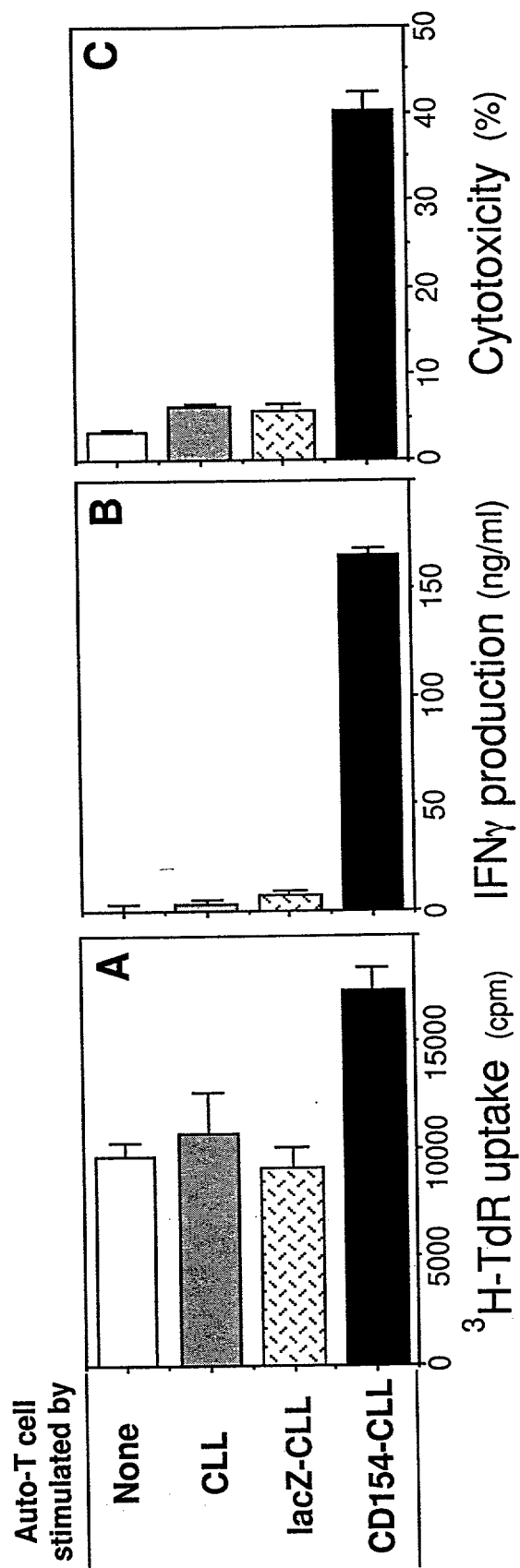


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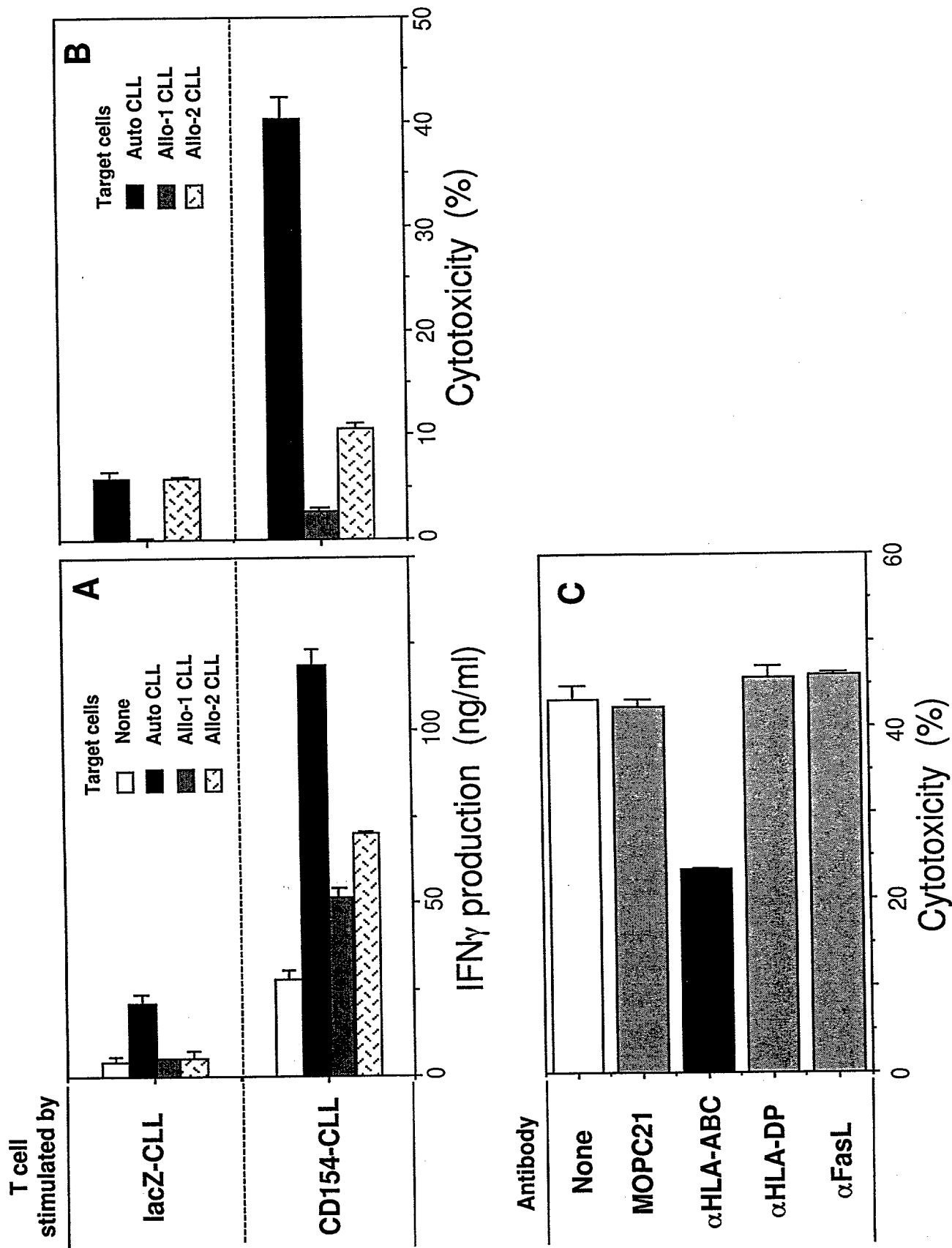


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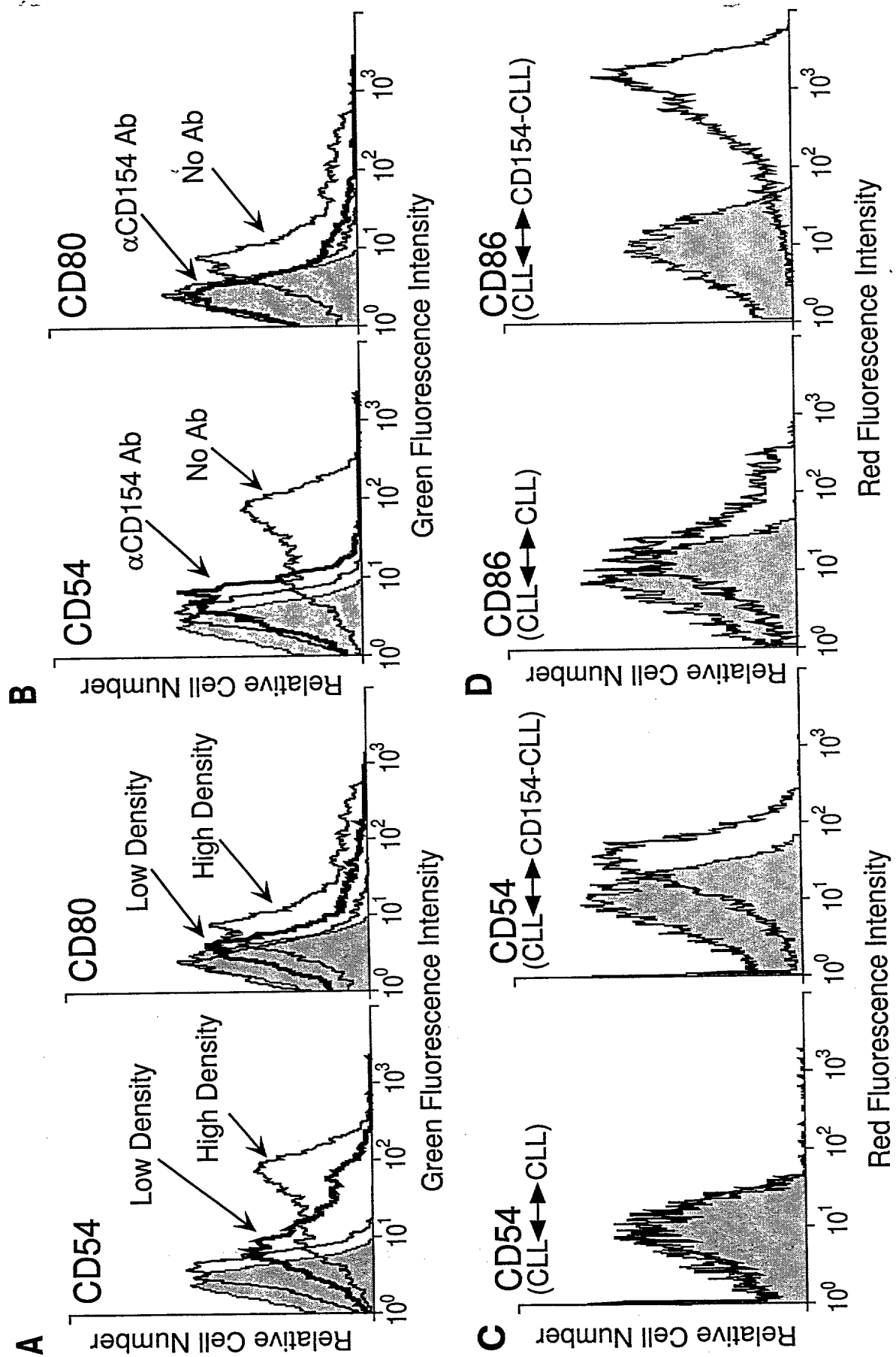


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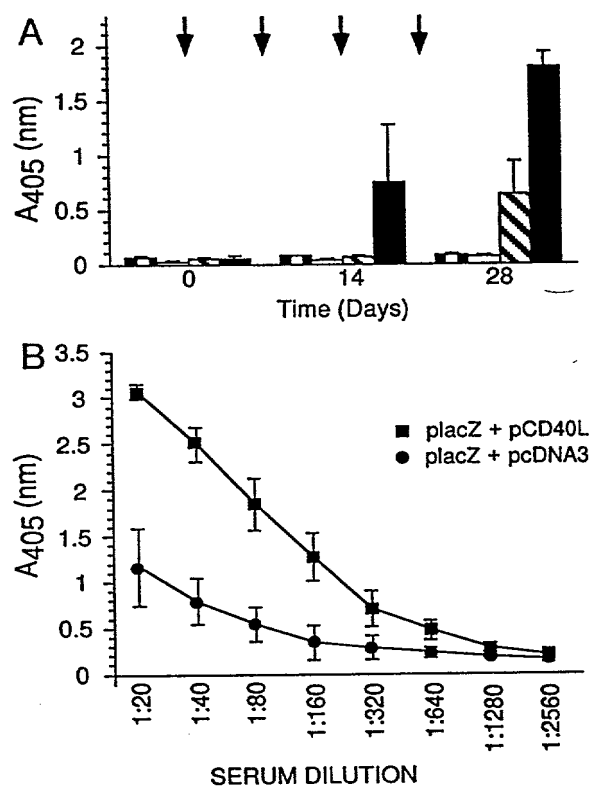


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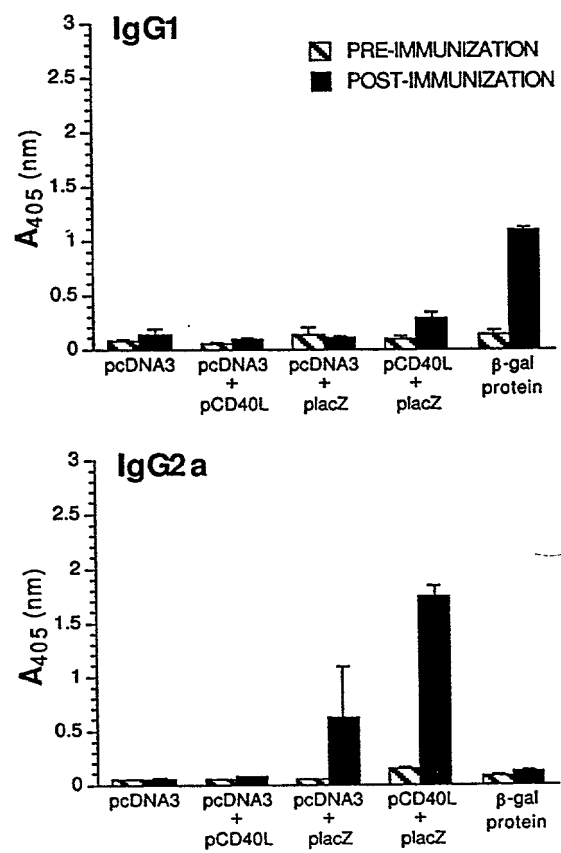


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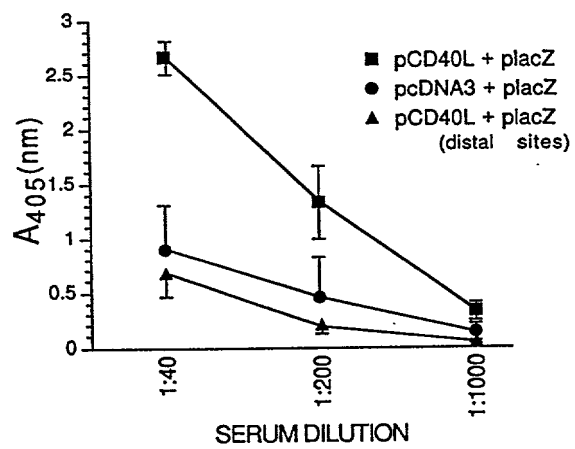


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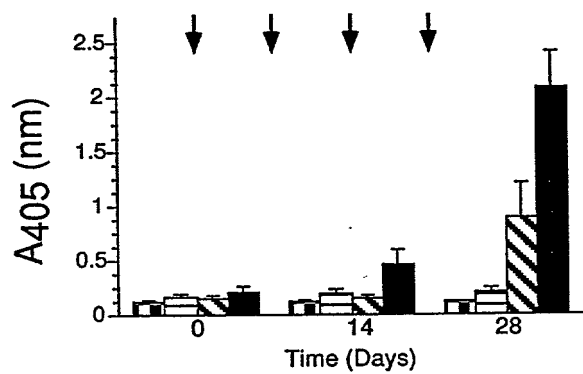


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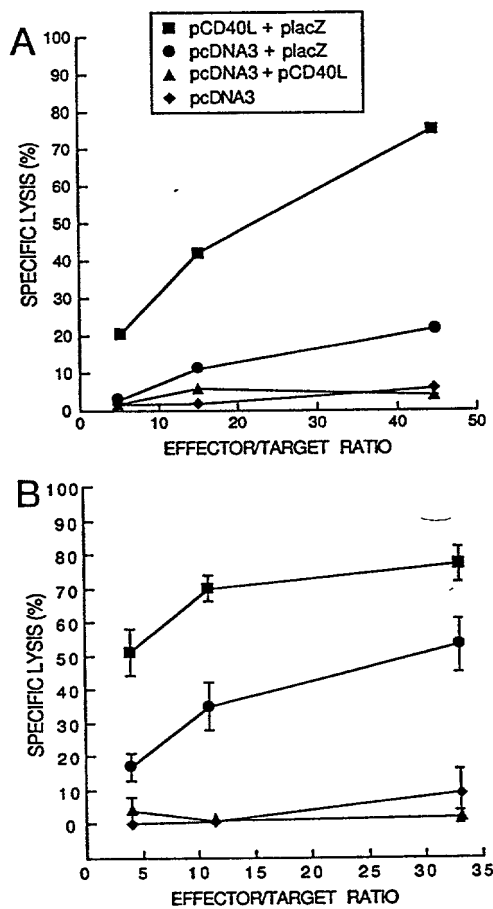


Figure 20

261021 222858

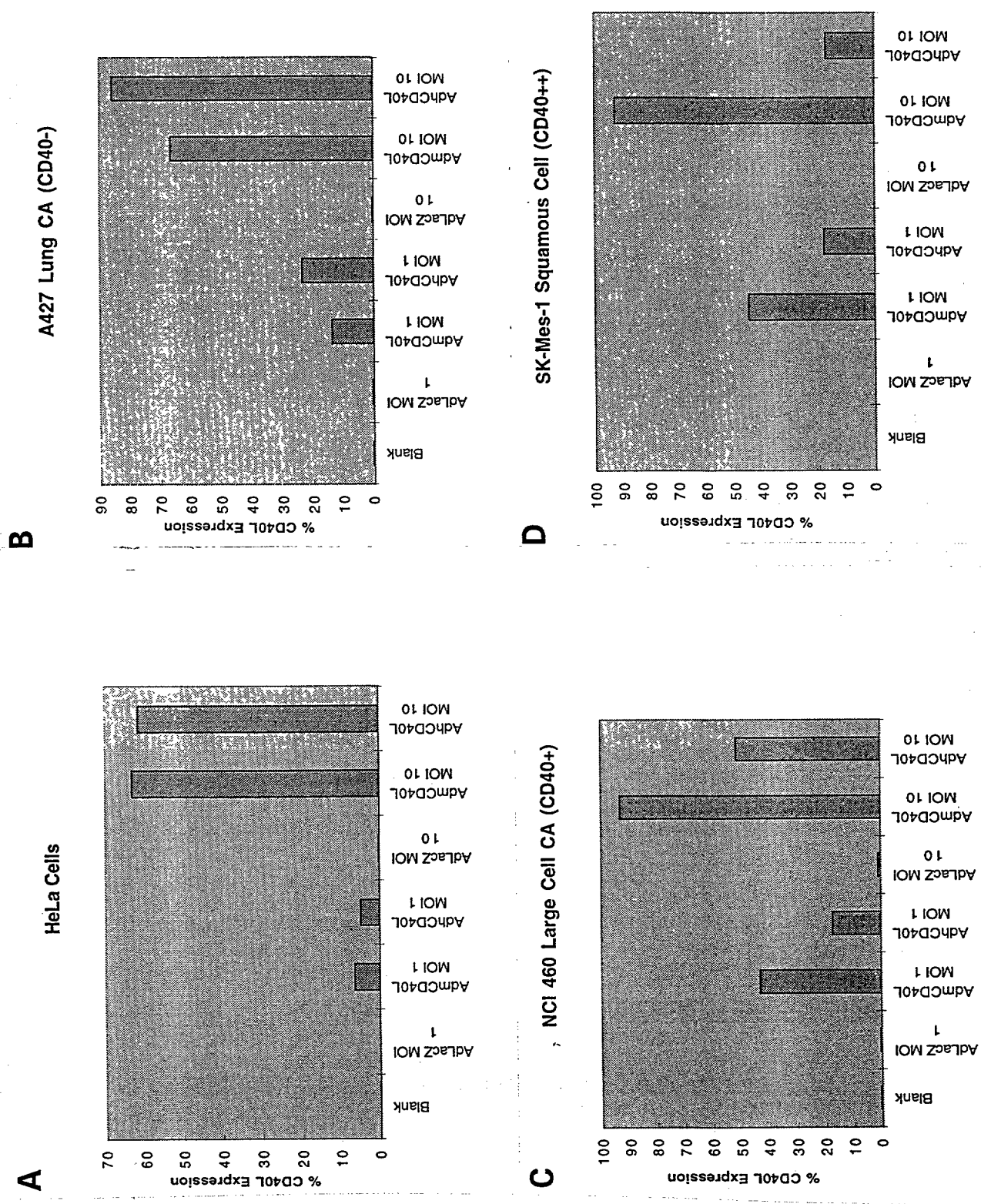
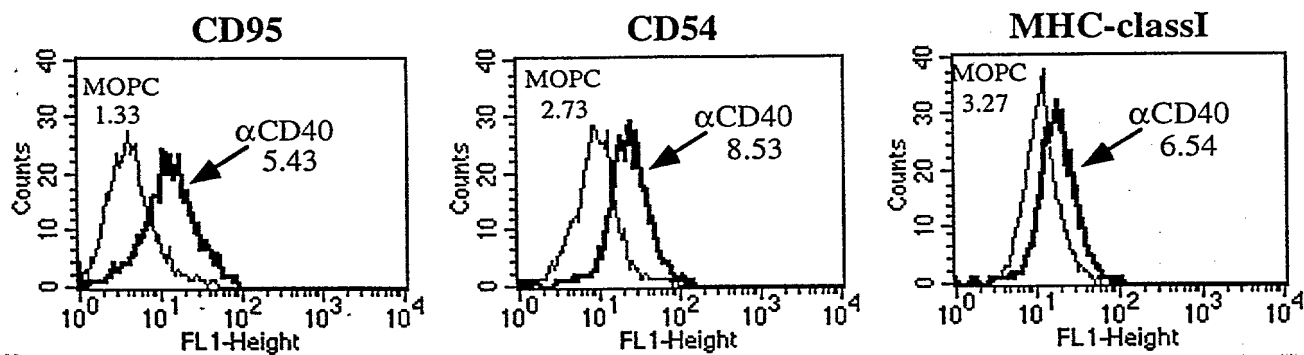


Figure 21

2228580

A



B

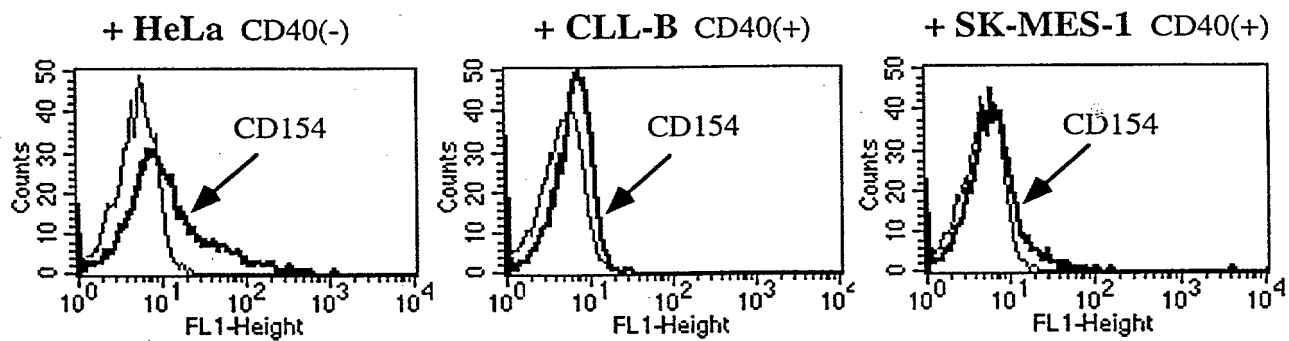


Figure 22

RA SYNOVIAL FLUID AND PLASMA INHIBITION OF FAS-LIGAND

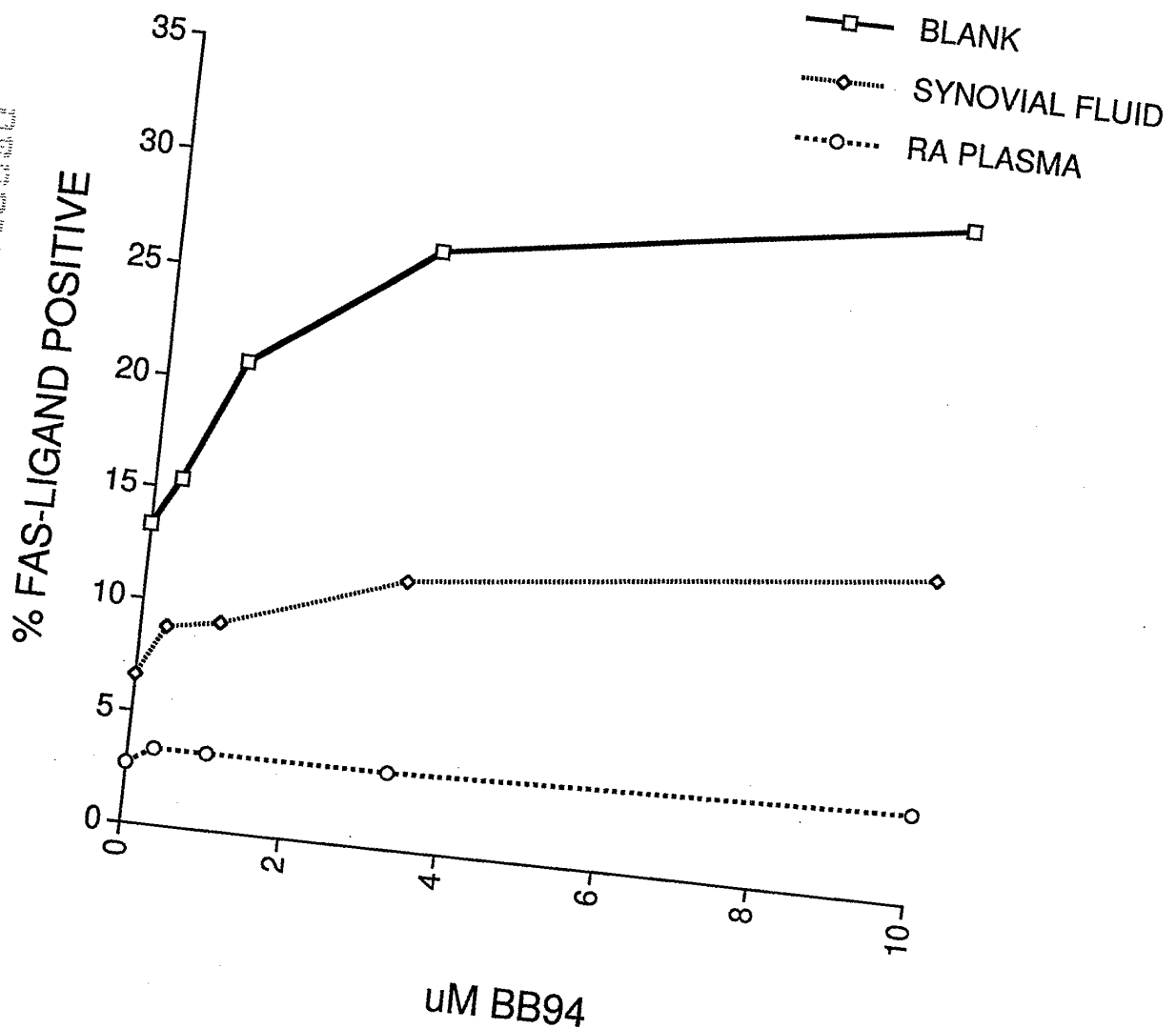


Figure 23

Gene Therapy of Leukemia

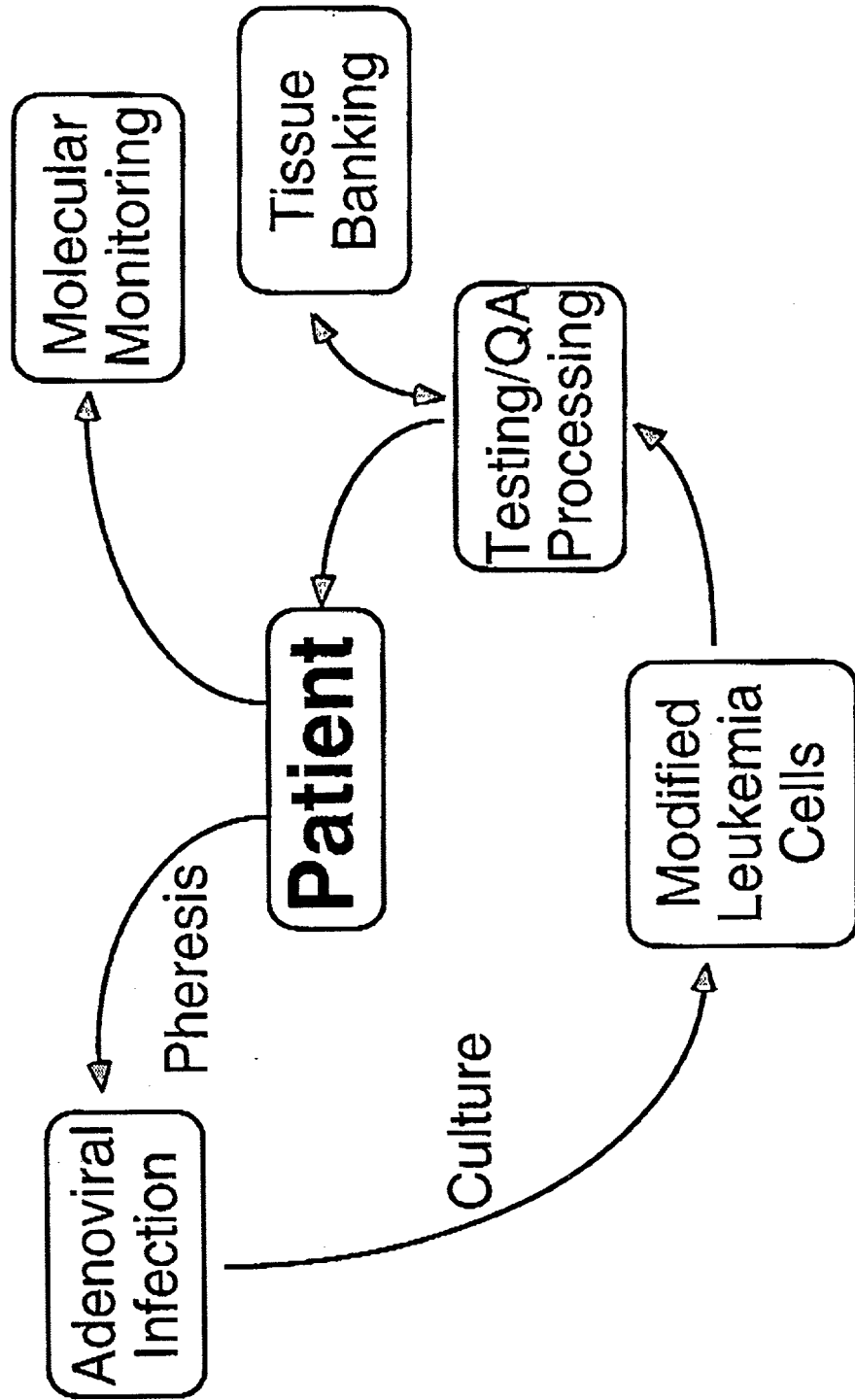


Figure 24

Matrix Metalloproteinase Cleavage Sites

Cleavage
↓

P₄ P₃ P₂ P₁ P'₁ P'₂ P'₃ P'₄

Collagenases

MMP-1 Interstitial Collagenase

P ₄	P ₃	P ₂	P ₁	P' ₁	P' ₂	P' ₃	P' ₄
Ala	Pro	Leu	Gly	Met	Arg	Met/Ala	Arg
Gly/Leu	Leu	Met/Tyr	His	Leu	Leu	Gly	Lys
Met	Ala	Val/Gly	Glu	Ile	Phe	Val	Gln
Glu	Asp	Ile	Tyr	Gln	Trp	Ser	Ile
Pro	Ser	Gln/Arg	Ala	Pro	Glu	Glu	Gly
Tyr	Glu	Asp	Phe	Phe	Ala	Phe	Ser
Ile	Gly	Glu	Gln	Ala	Val/Gly	Arg	Glu
Thr	Arg	Ala	Asn	Tyr/Val	Ser	Pro	Ala
Arg				[not K,E,W]	Asn		

MMP-8 Neutrophil Collagenase

P ₄	P ₃	P ₂	P ₁	P' ₁	P' ₂	P' ₃	P' ₄
Ala	Pro	Leu	Gly	Tyr	Ala	Gly	Arg
Gly/Leu	Leu	Gln	Gly/His	Ile	Leu	Met	Gln
Met			Ala	Leu	Trp	Ala	
Glu				Val			
Pro				Phe			
Tyr/Ile/Thr/Arg			Ala				
(otherwise same as MMP-1)							

Figure 28A

Gelatinases

MMP-2 Gelatinase A

P₄	P₃	P₂	P₁	P'₁	P'₂	P'₃	P'₄
Gly	Pro	Arg	Gly	Leu	Ala/Leu	Gly/Ala	Gln
Ile	Ala	Gln	Asn	Ile/Phe	Phe/Trp	Leu	Arg
Pro	Arg	Leu	Ala	Val/Met	Gly	Ser	His
Arg		Ala	His	Ala	Arg/Gln	Pro	Pro
Leu		Lys	Leu	Glu	His		
		Ile	Tyr	Gln/Asn	Val		
		His		Ser			

MMP-9 Gelatinase B

P₄	P₃	P₂	P₁	P'₁	P'₂	P'₃	P'₄
	Pro	Arg	Gly	Leu	Glu	Ala	Thr
		Gln		Ile/Phe	Ala/Leu/Phe	Leu	
Gln/Arg		Leu		Val/Met	Trp/Gly	Ser	
				Ala		Gly	

Stromelysins

MMP-3 Stromelysin 1

P₄	P₃	P₂	P₁	P'₁	P'₂	P'₃	P'₄
Asp	Pro	Phe	Glu	Leu	Arg	Ala	Thr
Gly	Ala	Leu/Met	Ala	Phe	Leu/Phe	Arg/Met	
Gln/Arg			Gln/Phe	Trp/Tyr	Trp	Gly	Pro
Leu	Val	Tyr	Asn	Ile	Val	Val/Ile	
Ile	Leu	Pro/Gly/Glu					
Glu/Val			His	Val	Gln	Ser/Asn	Ala
Leu	Ile		Gly	Met	His/Met	Glu/Thr	
Lys	Phe	Ala					
Gly/Asp		Ser	Leu/Pro	Glu	Glu/Ser/Thr	Leu	
Arg	Arg						
Ser/Lys/Phe			Lys/Tyr/Arg				
Pro/Met	Ser/Gly						
Ala/Phe/Gln							

Figure 28B

MMP-10	Stromelysin 2	P ₂ Ile His	P ₁ His Leu	P' ₁ Ile Leu	P' ₂ Gln Val	P' ₃ Ala Glu	P' ₄ Glu Ala
Others	Matrilysin	P ₂ Leu Gln Val	P ₁ Glu Met/Ala Pro/Gln Gly	P' ₁ Leu Ile Met	P' ₂ Arg Met Gln	P' ₃ Ala Val/Arg/Met Gly	P' ₄ Gln
MMP-7		P ₃ Pro Leu					

Figure 28C

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

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1
2
3 (1) General Information:
4
5
6 (i) APPLICANTS: Kipps, Thomas J.
7 Sharma, Sanjai
8 Cantwell, Mark
9
10
11 (ii) TITLE OF INVENTION: NOVEL EXPRESSION VECTORS
12 CONTAINING ACCESSORY
13 MOLECULE LIGAND GENES AND
14 THEIR USE FOR IMMUNO-
15 MODULATION AND TREATMENT OF
16 MALIGNANCIES
17
18
19 (iii) NUMBER OF SEQUENCES: 44
20
21
22 (iv) CORRESPONDENCE ADDRESS:
23
24 (A) ADDRESSEE: Lyon & Lyon
25 (B) STREET: 633 West Fifth Street
26 Suite 4700
27 (C) CITY: Los Angeles
28 (D) STATE: California
29 (E) COUNTRY: U.S.A.
30 (F) ZIP: 90071-2066
31
32
33 (v) COMPUTER READABLE FORM:
34
35 (A) MEDIUM TYPE: 3.5" Diskette,
36 1.44 Mb storage
37 (B) COMPUTER: IBM Compatible
38 (C) OPERATING SYSTEM: IBM P.C. DOS 5.0
39 (D) SOFTWARE: FastSeq Version 2.0
40
41
42
43 (vi) CURRENT APPLICATION DATA:
44
45 (A) APPLICATION NUMBER: To Be Assigned
46 (B) FILING DATE:

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47 (C) CLASSIFICATION:

48

49

50 (vii) PRIOR APPLICATION DATA:

51

52 (A) APPLICATION NUMBER: 60/132145

53 (B) FILING DATE: 12/9/96

54

55

56 (viii) ATTORNEY/AGENT INFORMATION:

57

58 (A) NAME: Guise, Jeffrey W.

59 (B) REGISTRATION NUMBER: 34,613

60 (C) REFERENCE/DOCKET NUMBER: 231/003

61

62

63 (ix) TELECOMMUNICATION INFORMATION:

64

65 (A) TELEPHONE: (213) 489-1600

66 (B) TELEFAX: (213) 955-0440

67 (C) TELEX: 67-3510

68

69

70 (2) INFORMATION FOR SEQ ID NO: 1:

71

72 (i) SEQUENCE CHARACTERISTICS:

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74 (A) LENGTH: 786 base pairs

75 (B) TYPE: nucleic acid

76 (C) STRANDEDNESS: single

77 (D) TOPOLOGY: linear

78

79 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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81 ATGATCGAAA CATAACAACCA AACCTCTCCC CGATCTGCGG CCACTGGACT GCCCATCAGC 60

82 ATGAAAAATTT TTATGTATTT ACTTACTGTT TTTCTTATCA CCCAGATGAT TGGGTCAGCA 120

83 CTTTTTGTCTG TGTATCTTCA TAGAAGGTTG GACAAGATAG AAGATGAAAG GAATCTTCAT 180

84 GAAGATTTTG TATTCATGAA AACGATACAG AGATGCAACA CAGGAGAAAG ATCCTTATCC 240

85 TTTACTGAAC TGTGAGGAGAT TAAAAGCCAG TTTGAAGGCT TTGTGAAGGA TATAATGTTA 300

86 AACAAAGAGG AGACGAAGAA AGAAAACAGC TTTGAAATGC AAAAAGGTGA TCAGAATCCT 360

87 CAAATTGCGG CACATGTCAT AAGTGAGGCC AGCAGTAAAA CAACATCTGT GTTACAGTGG 420

88 GCTGAAAAAG GATACTACAC CATGAGCAAC AACTTGGTAA CCCTGGAAAA TGGGAAACAG 480

89 CTGACCGTTA AAAGACAAGG ACTCTATTAT ATCTATGCCC AAGTCACCTT CTGTTCCAAT 540

90 CGGGAAGCTT CGAGTCAAGC TCCATTTATA GCCAGCCTCT GCCTAAAGTC CCCC GGTTAGA 600

91 TTCGAGAGAA TCTTACTCAG AGCTGCAAAT ACCACAGTT CCGCCAAACC TTGCGGGCAA 660

92 CAATCCATTC ACTTGGGAGG AGTATTTGAA TTGCAACCAG GTGCTTCGGT GTTTGTCAAT 720

93 GTGACTGATC CAAGCCAAGT GAGCCATGGC ACTGGCTTCA CGTCCTTTGG CTTACTCAAA 780

94 CTCTGA 786

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96

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98 (2) INFORMATION FOR SEQ ID NO: 2:

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102 (A) LENGTH: 783 base pairs
103 (B) TYPE: nucleic acid
104 (C) STRANDEDNESS: single
105 (D) TOPOLOGY: linear
106

107 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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110 ATGAAGATTT TTATGTATTT ACTTACTGTT TTCCTTATCA CCCAAATGAT TGGATCTGTG 120
111 CTTTTTGGCTG TGTATCTTCA TAGAAGATTG GATAAGGTCG AAGAGGAAGT AAACCTTCAT 180
112 GAAGATTTTG TATTCATAAA AAAGCTAAAG AGATGCAACA AAGGAGAAGG ATCTTTATCC 240
113 TTGCTGAACT GTGAGGAGAT GAGAAGGCAA TTTGAAGACC TTGTCAAGGA TATAACGTGA 300
114 AACAAAGAAG AGAAAAAGA AAACAGCTTT GAAATGCAAA GAGGTGATGA GGATCCTCAA 360
115 ATTGCAGCAC ACGTTGTAAG CGAAGCCAAC AGTAATGCAG CATCCGTTCT ACAGTGGGCC 420
116 AAGAAAGGAT ATTATACCAT GAAAAGCAAC TTGGTAATGC TTGAAAATGG GAAACAGCTG 480
117 ACGGTTAAAA GAGAAGGACT CTATTATGTC TACACTCAAG TCACCTTCTG CTCTAATCGG 540
118 GAGCCTTCGA GTCAACGCCC ATTCATCGTC GGCCTCTGGC TGAAGCCCAG CATTGGATCT 600
119 GAGAGAATCT TACTCAAGGC GGCAAATACC CACAGTTCCT CCCAGCTTTG CGAGCAGCAG 660
120 TCTGTTCACT TGGGCGGAGT GTTTGAATTA CAAGCTGGTG CTTCTGTGTT TGTCAACGTG 720
121 ACTGAAGCAA GCCAAGTGAT CCACAGAGTT GGCTTCTCAT CTTTGGCTT ACTCAAATC 780
122 TGA 783
123
124
125
126

127 (2) INFORMATION FOR SEQ ID NO: 3:

128 (i) SEQUENCE CHARACTERISTICS:

129
130
131 (A) LENGTH: 783 base pairs
132 (B) TYPE: nucleic acid
133 (C) STRANDEDNESS: single
134 (D) TOPOLOGY: linear
135

136 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

137
138 ATGATCGAAA CATAACACCA AACTTCTCCC CGATCTGCGG CCACTGGACT GCCCATCAGC 60
139 ATGAAAATTT TTATGTATTT ACTTACTGTT TTTCTTATCA CCCAGATGAT TGGGTCAGCA 120
140 CTTTTTGGCTG TGTATCTTCA TAGAAGATTG GATAAGGTCG AAGAGGAAGT AAACCTTCAT 180
141 GAAGATTTTG TATTCATAAA AAAGCTAAAG AGATGCAACA AAGGAGAAGG ATCTTTATCC 240
142 TTGCTGAACT GTGAGGAGAT GAGAAGGCAA TTTGAAGACC TTGTCAAGGA TATAACGTGA 300
143 AACAAAGAAG AGAAAAAGA AAACAGCTTT GAAATGCAAA GAGGTGATGA GGATCCTCAA 360
144 ATTGCAGCAC ACGTTGTAAG CGAAGCCAAC AGTAATGCAG CATCCGTTCT ACAGTGGGCC 420
145 AAGAAAGGAT ATTATACCAT GAAAAGCAAC TTGGTAATGC TTGAAAATGG GAAACAGCTG 480
146 ACGGTTAAAA GAGAAGGACT CTATTATGTC TACACTCAAG TCACCTTCTG CTCTAATCGG 540
147 GAGCCTTCGA GTCAACGCCC ATTCATCGTC GGCCTCTGGC TGAAGCCCAG CATTGGATCT 600
148 GAGAGAATCT TACTCAAGGC GGCAAATACC CACAGTTCCT CCCAGCTTTG CGAGCAGCAG 660
149 TCTGTTCACT TGGGCGGAGT GTTTGAATTA CAAGCTGGTG CTTCTGTGTT TGTCAACGTG 720
150 ACTGAAGCAA GCCAAGTGAT CCACAGAGTT GGCTTCTCAT CTTTGGCTT ACTCAAATC 780
151 TGA 783
152

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/982,272

DATE: 01/14/98

TIME: 16:27:38

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(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 786 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ATGATCGAAA	CATACAACCA	AACTTCTCCC	CGATCTGCGG	CCACTGGACT	GCCCATCAGC	60
ATGAAAATTT	TTATGTATTT	ACTTACTGTT	TTCCTTATCA	CCCAAATGAT	TGGATCTGTG	120
CTTTTTGCTG	TGTATCTTCA	TAGAAGGTTG	GACAAGATAG	AAGATGAAAG	GAATCTTCAT	180
GAAGATTTTG	TATTCATGAA	AACGATACAG	AGATGCAACA	CAGGAGAAAG	ATCCTTATCC	240
TTACTGAACT	GTGAGGAGAT	TAAAAGCCAG	TTTGAAGGCT	TTGTGAAGGA	TATAATGTTA	300
AACAAAGAGG	AGACGAAGAA	AGAAAACAGC	TTTGAATGTC	AAAAAGGTGA	TCAGAATCCT	360
CAAATTGCGG	CACATGTCAT	AAGTGAGGCC	AGCAGTAAAA	CAACATCTGT	GTTACAGTGG	420
GCTGAAAAAG	GATACTACAC	CATGAGCAAC	AACTTGGTAA	CCCTGGAAAA	TGGGAAACAG	480
CTGACCGTTA	AAAGACAAGG	ACTCTATTAT	ATCTATGCCC	AAGTCACCTT	CTGTTCCAAT	540
CGGGAAGCTT	CGAGTCAAGC	TCCATTTATA	GCCAGCCTCT	GCCTAAAGTC	CCCCGGTAGA	600
TTGAGAGAGAA	TCTTACTCAG	AGCTGCAAAT	ACCCACAGTT	CCGCCAAACC	TTGCGGGCAA	660
CAATCCATTC	ACTTGGGAGG	AGTATTTGAA	TTGCAACCAG	GTGCTTCGGT	GTTTGTCAAT	720
GTGACTGATC	CAAGCCAAGT	GAGCCATGGC	ACTGGCTTCA	CGTCCTTTGG	CTTACTCAAA	780
CTCTGA						786

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 783 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATGATCGAAA	CATACAACCA	AACTTCTCCC	CGATCTGCGG	CCACTGGACT	GCCCATCAGC	60
ATGAAAATTT	TTATGTATTT	ACTTACTGTT	TTCCTTATCA	CCCAAATGAT	TGGATCTGTG	120
CTTTTTGCTG	TGTATCTTCA	TAGAAGATTG	GATAAGGTCG	AAGAGGAAGT	AAACCTTCAT	180
GAAGATTTTG	TATTCATAAA	AAAGCTAAAG	AGATGCAACA	AAGGAGAAGG	ATCTTTATCC	240
TTGCTGAACT	GTGAGGAGAT	GAGAAGGCAA	TTTGAAGACC	TTGTCAAGGA	TATAACGTTA	300
AACAAAGAAG	AGAAAAAAGA	AAACAGCTTT	GAAATGCAAA	GAGGTGATGA	GGATCCTCAA	360
ATTGCAGCAC	ACGTTGTAAG	CGAAGCCAAC	AGTAATGCAG	CATCCGTTCT	ACAGTGGGCC	420
AAGAAAGGAT	ATTATACCAT	GAAAAGCAAC	TTGGTAATGC	TTGAAAATGG	GAAACAGCTG	480
ACGGTTAAAA	GAGAAGGACT	CTATTATGTC	TACACTCAAG	TCACCTTCTG	CTCTAATCGG	540
GAGCCTTCGA	GTCAACGCC	ATTTCATCGTC	GGCCTCTGGC	TGAAGCCCAG	CATTGGATCT	600
GAGAGAATCT	TACTCAAGGC	GGCAAATACC	CACAGTTCCT	CCCAGCTTTG	CGAGCAGCAG	660
TCTGTTCACT	TGGGCGGAGT	GTTTGAATTA	CAAGCTGGTG	CTTCTGTGTT	TGTCAACGTG	720

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PATENT APPLICATION US/08/982,272

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206 ACTGAAGCAA GCCAAGTGAT CCACAGAGTT GGCTTCTCAT CTTTGGCTT ACTCAAATC 780
207 TGA 783
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210

211 (2) INFORMATION FOR SEQ ID NO: 6:
212

213 (i) SEQUENCE CHARACTERISTICS:
214

215 (A) LENGTH: 786 base pairs
216 (B) TYPE: nucleic acid
217 (C) STRANDEDNESS: single
218 (D) TOPOLOGY: linear
219

220 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
221

222 ATGATAGAAA CATAAGCCCA ACCTTCCCCC AGATCCGTGG CAACTGGACT TCCAGCGAGC 60
223 ATGAAGATTT TTATGTATTT ACTTACTGTT TTTCTTATCA CCCAGATGAT TGGGTCAGCA 120
224 CTTTTTGCTG TGTATCTTCA TAGAAGGTTG GACAAGATAG AAGATGAAAG GAATCTTCAT 180
225 GAAGATTTTG TATTCATGAA AACGATACAG AGATGCAACA CAGGAGAAAG ATCCTTATCC 240
226 TTTACTGAACT GTGAGGAGAT TAAAAGCCAG TTTGAAGGCT TTGTGAAGGA TATAATGTTA 300
227 AACAAAGAGG AGACGAAGAA AGAAAACAGC TTTGAAATGC AAAAAGGTGA TCAGAAATCCT 360
228 CAAATTGCGG CACATGTCAT AAGTGAGGCC AGCAGTAAAA CAACATCTGT GTTACAGTGG 420
229 GCTGAAAAAG GATACTACAC CATGAGCAAC AACTTGGTAA CCCTGGAAAA TGGGAAACAG 480
230 CTGACCGTTA AAAGACAAGG ACTCTATTAT ATCTATGCCC AAGTCACCTT CTGTTCCAAT 540
231 CGGGAAGCTT CGAGTCAAGC TCCATTTATA GCCAGCCTCT GCCTAAAGTC CCCCAGTAGA 600
232 TTCGAGAGAA TCTTACTCAG AGCTGCAAAT ACCACAGTT CCGCCAAACC TTGCGGGCAA 660
233 CAATCCATTC ACTTGGGAGG AGTATTTGAA TTGCAACCAG GTGCTTCGGT GTTTGTCAAT 720
234 GTGACTGATC CAAGCCAAGT GAGCCATGGC ACTGGCTTCA CGTCCTTTGG CTTACTCAAA 780
235 CTCTGA 786
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245 (2) INFORMATION FOR SEQ ID NO: 7:
246

247 (i) SEQUENCE CHARACTERISTICS:
248

249 (A) LENGTH: 786 base pairs
250 (B) TYPE: nucleic acid
251 (C) STRANDEDNESS: single
252 (D) TOPOLOGY: linear
253

254 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
255

256 ATGATAGAAA CATAAGCCCA ACCTTCCCCC AGATCCGTGG CAACTGGACT TCCAGCGAGC 60
257 ATGAAGATTT TTATGTATTT ACTTACTGTT TTTCTTATCA CCCAAATGAT TGGATCTGTG 120
258 CTTTTTGCTG TGTATCTTCA TAGAAGGTTG GACAAGATAG AAGATGAAAG GAATCTTCAT 180

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/982,272

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Line	Error	Original Text
45	Wrong application Serial Number	(A) APPLICATION NUMBER: To Be Assigned

2008/01/14 16:27:46